

From: Bunner, Bridget
Sent: Wednesday, May 11, 2005 9:43 AM
To: STIC-Biotech/ChemLib
Subject: sequence search request

Hi! I'd like to request a sequence search for case 10/649,952:

1. the amino acid sequence of SEQ ID NO: 2
2. the amino acid sequence encoded by SEQ ID NO: 1

Thanks!

Bridget Bunner

Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: 5/13 _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____ •

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2005, 09:41:10 ; Search time 134 Seconds
(without alignments)
413.825 Million cell updates/sec

Title: US-10-649-952A-1
Perfect score: 846
Sequence: 1 MASGVAVSDGVIKFVNDMKV.....CTLAELKGGSAVISLEGKPL 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

- 1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
- 3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
- 13: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
- 18: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	846	100.0	166	16	US-10-649-952A-1
2	764	90.3	149	16	US-10-408-765A-2270
3	702	83.0	166	14	US-10-205-342-21
4	699	82.6	166	14	US-10-205-823-72
5	699	82.6	166	16	US-10-408-765A-1910
6	699	82.6	205	15	US-10-158-034-93
7	557.5	65.9	149	16	US-10-408-765A-2351
8	460	54.4	129	15	US-10-158-034-94
9	450	53.2	156	15	US-10-158-034-68
10	273	32.3	106	15	US-10-264-049-4340
11	267.5	31.6	143	15	US-10-369-493-2293
12	253.5	30.0	141	16	US-10-263-255-2
13	245.5	29.0	141	16	US-10-263-255-4

14	239.5	28.3	139	15	US-10-424-599-186070
15	230	27.2	60	14	US-10-029-386-30107
16	230	27.2	190	15	US-10-369-493-2272
17	227	26.8	145	15	US-10-425-114-37040
18	227	26.8	161	15	US-10-425-114-59591
19	227	26.8	171	15	US-10-425-114-39098
20	227	26.8	179	15	US-10-425-114-38879
21	227	26.8	179	15	US-10-425-114-41223
22	227	26.8	179	15	US-10-425-114-44883
23	227	26.8	179	15	US-10-425-114-51312
24	227	26.8	179	15	US-10-425-114-57582
25	227	26.8	179	15	US-10-425-114-59194
26	227	26.8	179	15	US-10-425-114-59883
27	227	26.8	179	15	US-10-425-114-66714
28	227	26.8	179	15	US-10-425-114-67765
29	227	26.8	179	15	US-10-425-114-72052
30	227	26.8	179	15	US-10-425-114-72097
31	224.5	26.5	139	16	US-10-767-701-45854
32	223.5	26.4	194	16	US-10-767-701-43979
33	221	26.1	139	15	US-10-250-613-9
34	221	26.1	157	15	US-10-425-114-59062
35	221	26.1	173	15	US-10-425-114-66010
36	221	26.1	176	15	US-10-425-114-69864
37	221	26.1	177	15	US-10-425-114-44953
38	221	26.1	177	15	US-10-425-114-48026
39	221	26.1	177	15	US-10-425-114-48329
40	221	26.1	177	15	US-10-425-114-49519
41	221	26.1	177	15	US-10-425-114-53265
42	221	26.1	177	15	US-10-425-114-53325
43	221	26.1	177	15	US-10-425-114-66577
44	221	26.1	177	15	US-10-425-114-66602
45	221	26.1	181	15	US-10-425-114-69951

ALIGNMENTS

RESULT 1
US-10-649-952A-1
; Sequence 1, Application US/10649952A
; Publication No. US20040157326A1
; GENERAL INFORMATION:
; APPLICANT: DAIICHI SUNTORY PHARMA CO., LTD.
; APPLICANT: Daiichi Suntory Biomedical Research Ltd.
; APPLICANT: Miura, Kenji
; APPLICANT: Haruyama, Munetada
; APPLICANT: Kodama, Shiko
; TITLE OF INVENTION: Promoters of the growth and/or differentiation of hematopoietic stem cells and/or hematopoietic progenitors
; FILE OF INVENTION: 58777.000013
; CURRENT APPLICATION NUMBER: US/10/649,952A
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: PCT/JPO2/13862
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: JAPAN 400330/2001
; PRIOR FILING DATE: 2001-12-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Human
US-10-649-952A-1

Query Match 100.0%; Score 846; DB 16; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-76;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGVAVSDGVTKFVNDMKVKSSTPEEVKKKKAVLFCLSDDKNNIILEGKEILVGV 60
Db 1 MASGVAVSDGVTKFVNDMKVKSSTPEEVKKKKAVLFCLSDDKNNIILEGKEILVGV 60
QY 61 GQVDDPVATFVKMLPKDKCRYALDYATYETKESKKDLVFIWAPESAPLKSMMIYASS 120

Db 61 GQTVDDPYATFVKMLPDKOCRYALYDATYETKESKKEDLVFIWAPESAPLKSMIYASS 120
Qy 121 KDAIKKKLTGKIKHELQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166
Db 121 KDAIKKKLTGKIKHELQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166

RESULT 2

US-10-408-765A-2270
; Sequence 2270, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408.765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2270
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2270

Query Match 90.3%; Score 764; DB 16; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.9e-68;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MKVKRSTPTEVKRKKKAVLFCISEDKKNIILLEGKILVGDVGQTVDDPYATFVKMLPD 77
Db 1 MKVKRSTPTEVKRKKKAVLFCISEDKKNIILLEGKILVGDVGQTVDDPYATFVKMLPD 60
Qy 78 KOCRYALYDATYETKESKKEDLVFIWAPESAPLKSMIYASSKDAIKKKLTGKIKHELQA 137
Db 61 KOCRYALYDATYETKESKKEDLVFIWAPESAPLKSMIYASSKDAIKKKLTGKIKHELQA 120
Qy 138 NCYEEVKDRCTLAELKGGSAVISLEGKPL 166
Db 121 NCYEEVKDRCTLAELKGGSAVISLEGKPL 149

RESULT 3

US-10-205-342-21
; Sequence 21, Application US/10205342
; Publication No. US20030108906A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brookesbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018198
; CURRENT APPLICATION NUMBER: US/10/205.342
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:

; OTHER INFORMATION: Protein: Cofilin
US-10-205-342-21

Query Match 83.0%; Score 702; DB 14; Length 166;
Best Local Similarity 81.3%; Pred. No. 3.5e-62;
Matches 135; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MASGAVSDGVIKVFNDMKVRKSTPTEVKRKKKAVLFCISEDKKNIILLEGKILVGDV 60
Db 1 MASGVTVNDDEVIKVFNDMKVRKSTQEEIKRKKKAVLFCISDDKQRIIVEAKQILVGD 60
Qy 61 GQTVDDPYATFVKMLPDKOCRYALYDATYETKESKKEDLVFIWAPESAPLKSMIYASS 120
Db 61 GQTVDDPYATFVKMLPDKOCRYALYDATYETKESKKEDLVFIWAPESAPLKSMIYASS 120
Qy 121 KDAIKKKLTGKIKHELQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166
Db 121 KDAIKKKLTGKIKHEWQVNGLDIDKDRSTLGEKLGSSVVVSLEGKPL 166

RESULT 4

US-10-205-823-72
; Sequence 72, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205.823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-72

Query Match 82.6%; Score 699; DB 14; Length 166;
Best Local Similarity 80.7%; Pred. No. 7.1e-62;
Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MASGAVSDGVIKVFNDMKVRKSTPTEVKRKKKAVLFCISEDKKNIILLEGKILVGDV 60
Db 1 MASGVTVNDDEVIKVFNDMKVRKSTQEEIKRKKKAVLFCISDDKQRIIVEAKQILVGD 60
Qy 61 GQTVDDPYATFVKMLPDKOCRYALYDATYETKESKKEDLVFIWAPESAPLKSMIYASS 120
Db 61 GQTVDDPYATFVKMLPDKOCRYALYDATYETKESKKEDLVFIWAPESAPLKSMIYASS 120
Qy 121 KDAIKKKLTGKIKHELQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166

Db 121 KDAIKKKFTGIRKHEWQVNGLLDKDRSTLGEKLGKGNVVSLEKPL 166

RESULT 5
US-10-408-765A-1910
; Sequence 1910, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1910
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1910

Query Match 82.6%; Score 699; DB 16; Length 166;
Best Local Similarity 80.7%; Pred. No. 7.1e-62;
Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 MASGVAVSGVIVKFNMDKVRKSTPEEVKKRKAFLCLSDKKNIIIEEGKEILVGDV 60
DB 1 MASGVTNDEVIVKFNMDKVRKSTPEEVKKRKAFLCLSDKKNIIIEEGKEILVGDV 60
QY 61 GOTVDDPYATFVKMLPDKCRYALYDATYETKESKEDLVFIFWAPESAPLKSMMIYASS 120
DB 61 GOTVEDPYTSFVKLLPLNDCRYALYDATYETKESKEDLVFIFWAPESAPLKSMMIYASS 120
QY 121 KDAIKKKFTGIRKHEWQVNGLLDKDRSTLGEKLGKGNVVSLEKPL 166
DB 121 KDAIKKKFTGIRKHEWQVNGLLDKDRSTLGEKLGKGNVVSLEKPL 166

RESULT 6
US-10-158-034-93
; Sequence 93, Application US/10158034
; Publication No. US20030219758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT210C1
; CURRENT APPLICATION NUMBER: US/10/158,034
; CURRENT FILING DATE: 2002-05-31
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-034-93

Query Match 82.6%; Score 699; DB 15; Length 205;
Best Local Similarity 80.7%; Pred. No. 9.4e-62;
Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 MASGVAVSGVIVKFNMDKVRKSTPEEVKKRKAFLCLSDKKNIIIEEGKEILVGDV 60
DB 40 MASGVTNDEVIVKFNMDKVRKSTPEEVKKRKAFLCLSDKKNIIIEEGKEILVGDV 99

QY 61 GOTVDDPYATFVKMLPDKCRYALYDATYETKESKEDLVFIFWAPESAPLKSMMIYASS 120
DB 100 GOTVEDPYTSFVKLLPLNDCRYALYDATYETKESKEDLVFIFWAPESAPLKSMMIYASS 159
QY 121 KDAIKKKFTGIRKHEWQVNGLLDKDRSTLGEKLGKGNVVSLEKPL 166
DB 160 KDAIKKKFTGIRKHEWQVNGLLDKDRSTLGEKLGKGNVVSLEKPL 205

RESULT 7
US-10-408-765A-2351
; Sequence 2351, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2351
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2351

Query Match 65.9%; Score 557.5; DB 16; Length 148;
Best Local Similarity 72.5%; Pred. No. 9e-48; Indels 1; Gaps 1;
Matches 108; Conservative 18; Mismatches 22;

QY 18 MKVRKSTPEEVKKRKAFLCLSDKKNIIIEEGKEILVGDVGTVDPPYATFVKMLPD 77
DB 1 MKVRKSTPEEVKKRKAFLCLSDKKNIIIEEGKEILVGDVGTVDPPYATFVKMLPD 60
QY 78 KDCRYALYDATYETKESKEDLVFIFWAPESAPLKSMMIYASSKDAIKKLTGIRKHELOA 137
DB 61 KDCRYALYDASPTKESRKEELMFLWAPELAPLKSMMIYASSKDAIKKLTGIRKHELOA 120
QY 138 NCYEEVKDRCTLAELKGGSAVISLEKPL 166
DB 121 NGPEDLNRACTLAELKGGSLIVAFEGCPV 148

RESULT 8
US-10-158-034-94
; Sequence 94, Application US/10158034
; Publication No. US20030219758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT210C1
; CURRENT APPLICATION NUMBER: US/10/158,034
; CURRENT FILING DATE: 2002-05-31
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (107)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:

; NAME/KEY: misc feature
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (126)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (127)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (128)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-158-034-94

Query Match 54.4%; Score 460; DB 15; Length 129;
Best Local Similarity 81.3%; Pred. No. 4.4e-38;
Matches 87; Conservative 10; Mismatches 10; Indels 0; Gaps 0;
Qy 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSDKKNILLEGKEILVGDV 60
Db 13 MASGVTNDEVIKVFNDKVRKSTQBEIKRKAVALFCLSDKKNILLEGKEILVGDV 72
Qy 61 GQTVDDPYATFVKMLPKDCKRYALYDATYETKSKEDLVFIWAPESAPL 107
Db 73 GDTVEDPYTSFVKLLPLNDCKRYALYDATYETKSKEDLVFIWAPESAPL 119

RESULT 9

US-10-158-034-68
; Sequence 68, Application US/10158034
; Publication No. US20030219759A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ10C1
; CURRENT APPLICATION NUMBER: US/10/158,034
; CURRENT FILING DATE: 2002-05-31
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 68
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-034-68

Query Match 53.2%; Score 450; DB 15; Length 156;
Best Local Similarity 81.7%; Pred. No. 5.7e-37;
Matches 85; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSDKKNILLEGKEILVGDV 60
Db 45 MASGVTNDEVIKVFNDKVRKSTQBEIKRKAVALFCLSDKKNILLEGKEILVGDV 104
Qy 61 GQTVDDPYATFVKMLPKDCKRYALYDATYETKSKEDLVFIWAPESAPL 104
Db 105 GDTVEDPYTSFVKLLPLNDCKRYALYDATYETKSKEDLVFIWAPESAPL 148

RESULT 10

US-10-264-049-4340
; Sequence 4340, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569

; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patent In Ver. 3.1
; SEQ ID NO 4340
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (91)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (100)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4340

Query Match 32.1%; Score 273; DB 15; Length 106;
Best Local Similarity 55.2%; Pred. No. 1.8e-19;
Matches 58; Conservative 13; Mismatches 34; Indels 0; Gaps 0;
Qy 8 SDGVKVFNDKVRKSTPEEVKKRKAVALFCLSDKKNILLEGKEILVGDVQTVDDP 67
Db 1 ADEVCRIFYDMKVRKSTPEEVKKRKAVALFCLSDKKNILLEGKEILVGDVQTVDDP 60
Qy 68 YATFVKMLPKDCKRYALYDATYETKSKEDLVFIWAPESAPL 112
Db 61 FKHFVGMLLKKIVAMLCMQLKQKSEKKLMPFWGAPXLTGFK 105

RESULT 11

US-10-369-493-22293
; Sequence 22293, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkie, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22293
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22293

Query Match 31.6%; Score 267.5; DB 15; Length 143;
Best Local Similarity 37.8%; Pred. No. 9.6e-19;
Matches 54; Conservative 31; Mismatches 37; Indels 21; Gaps 3;
Qy 3 SGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSDKKNILLEGKEILVGDVQ 62
Db 4 SGVAVADESLTAFNDLK-----LGKKYKILGLNDKATEIVVKE-----T 44
Qy 63 TVDDPYATFVKMLPKDCKRYALYDATYET--KSKEDLVFIWAPESAPLKSMTYASS 120
Db 45 STDPDYDAFLEKLPENDCLYALYDFEYINGEGKRSKIVFTWSPDTAPVRSKMYASS 104
Qy 121 KDAIKKLTGKIKHELQANCYEEV 143
Db 105 KDALRRALNGVSTDVQGTDFSEV 127


```
RESULT 12
US-10-263-255-2
; Sequence 2, Application US/10263255
; Publication No. US20040191771A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Chua, Penelope
; APPLICANT: Nislow, Corey
; TITLE OF INVENTION: Candida Albicans Cofilin
; FILE REFERENCE: CYTOPO72
; CURRENT APPLICATION NUMBER: US/10/263,255
; CURRENT FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Candida Albicans
US-10-263-255-2

Query Match      30.0%; Score 253.5; DB 16; Length 141;
Best Local Similarity 33.6%; Pred. No. 2.4e-17;
Matches 48; Conservative 38; Mismatches 36; Indels 21; Gaps 3;

QY 3 SGVAVSDGVKVPNDMKVRKSTPPEVKRKKAVLFCLSDEKKNIILEGKEILVGDVGQ 62
DB 4 SGTVADESILTAFLDK-----LGRKYKFIPLNDEKTIIVSEQ-----T 44

QY 63 TVDDPVATFVKMLPKDKCRYALYDATYET--KESKKEDLVFIWAPESAPLKSMMIYASS 120
DB 45 STEQEYDAFLEKLPENECHYAVDYFDYDYGGEGRKSKIVFFTWSPDTAPVRAKMWYASS 104

QY 121 KDAIKKKLTGKIKHELQANCYEEV 143
DB 105 KDSLRALNGVAADVQGTDFSEV 127

RESULT 13
US-10-263-255-4
; Sequence 4, Application US/10263255
; Publication No. US20040191771A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Chua, Penelope
; APPLICANT: Nislow, Corey
; TITLE OF INVENTION: Candida Albicans Cofilin
; FILE REFERENCE: CYTOPO72
; CURRENT APPLICATION NUMBER: US/10/263,255
; CURRENT FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-263-255-4

Query Match      29.0%; Score 245.5; DB 16; Length 141;
Best Local Similarity 33.6%; Pred. No. 1.5e-16;
Matches 48; Conservative 37; Mismatches 37; Indels 21; Gaps 3;

QY 3 SGVAVSDGVKVPNDMKVRKSTPPEVKRKKAVLFCLSDEKKNIILEGKEILVGDVGQ 62
DB 4 SGTVADESILTAFLDK-----LGRKYKFIPLNDEKTIIVSEQ-----T 44

QY 63 TVDDPVATFVKMLPKDKCRYALYDATYET--KESKKEDLVFIWAPESAPLKSMMIYASS 120
DB 45 STEQEYDAFLEKLPENECHYAVDYFDYDYGGEGRKSKIVFFTWSPDTAPVRAKMWYASS 104

QY 121 KDAIKKKLTGKIKHELQANCYEEV 143
DB 105 KDFLRALNGVAADVQGTDFFEV 127
```

```
RESULT 14
US-10-424-599-186070
; Sequence 186070, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(S3223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 186070
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139033C.1.pep
US-10-424-599-186070

Query Match      28.3%; Score 239.5; DB 15; Length 139;
Best Local Similarity 34.9%; Pred. No. 5.9e-16;
Matches 52; Conservative 27; Mismatches 51; Indels 19; Gaps 3;

QY 3 SGVAVSDGVKVPNDMKVRKSTPPEVKRKKAVLFCLSDEKKNIILEGKEILVGDVGQ 62
DB 4 TGIADVNECVNEFNAPKLRNT-----HRYIVF-----KIENAKEIKIKKGE 45

QY 63 TVDDPVATFVKMLPKDKCRYALYDATYETKESKKEDLVFIWAPESAPLKSMMIYASSKD 122
DB 46 TTAS-YDFLKQLPNDCHYAVYNEYNQADGFRSKIVFLWAPDTAPTKSKMLYAGTKD 104

QY 123 AIKKKLTGKIKHELQANCYEEVKDRCITLAE 151
DB 105 TLKKNLQGLQVEMQGTDKSEVDQSEVLAK 133

RESULT 15
US-10-029-386-30107
; Sequence 30107, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30107
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL132765.16
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.9
; OTHER INFORMATION: SWISSPROT HIT: P18282, EVALUUE 1.00e-29
US-10-029-386-30107

Query Match      27.2%; Score 230; DB 14; Length 60;
Best Local Similarity 74.1%; Pred. No. 1.7e-15;
Matches 43; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 44 KKNIILEGKEILVGDVGQTVDDPVATFVKMLPKDKCRYALYDATYETKESKKEDLVF 101
```

Db 1 KKCIIVEEGKEILVGDVGWTTITDPFKHFVGMPLPEKDCRYALYDASFETKESRKEELMP 58

Search completed: May 13, 2005, 09:50:41
Job time : 135 secs

Result No.	Query No.	Score	Match	Length	DB	ID	Description	§
1	846	100.0	166	5	AB981882	Human cof		
2	846	100.0	166	6	ADA37012	Human cof		
3	846	100.0	166	8	AD124535	Human mcd		
4	846	100.0	166	8	ADO05889	Human cof		
5	846	100.0	166	8	ADQ30534	Pancreas		
6	846	100.0	229	8	ADQ65133	Novel hum		
7	842	99.5	187	6	ABR41637	Human DIT		
8	841	99.4 *	239	8	ADN99790	Novel hum		
9	764	90.3	149	7	ADJ70464	Human hea		
10	702	83.0	166	6	ABR41956	Mouse cof		
11	699	82.6	166	4	AAW78545	Human pro		
12	699	82.6	166	7	ADB75248	Prostate		
13	699	82.6	166	7	ADJ70104	Human hea		
14	699	82.6	166	8	AD124536	Human mod		
15	699	82.6	205	4	AAU18546	Human cyt		
16	699	82.6	207	4	AAW79529	Human pro		
17	666.5	78.8	154	8	ADN99460	Novel hum		
18	645.5	76.3	153	8	ADN99430	Novel hum		
19	616	72.8	127	3	AAQ03978	Human sec		
20	606.5	71.7	165	3	AAQ03876	Human sec		
21	606.5	71.7	165	4	AAW40267	Human pol		
22	606.5	71.7	165	8	AD124537	Human mod		
23	606.5	71.7	165	8	ADQ30570	Pancreas		
24	606.5	71.7	188	8	ADP23096	PRO polyp		
25	606.5	71.7	188	4	AAW42053	Human polyp		

CC invention
XX Sequence 166 AA;
SQ Query Match 100.0%; Score 846; DB 5; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSEDKKNIIIEGKEILVGDV 60
Db 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSEDKKNIIIEGKEILVGDV 60
Qy 61 GOTVDDPYATFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMIYASS 120
Db 61 GOTVDDPYATFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMIYASS 120
Qy 121 KDAIKKKLTGKHELOQANCYEEVKDRCTLAELGSSAVISLEGKPL 166
Db 121 KDAIKKKLTGKHELOQANCYEEVKDRCTLAELGSSAVISLEGKPL 166

RESULT 2
ADA37012
ID ADA37012 standard; protein; 166 AA.
XX
AC ADA37012;
DT 20-NOV-2003 (first entry)
DE Human cofillin protein SEQ ID NO:1.
XX
KW proliferation; differentiation; haematopoietic stem cell; cofillin;
KW vasotropic; antianaemic; cytostatic; vulnerable; nephrotropic;
KW hepatotropic; haematopoietic hypofunction; Fanconi's disease;
KW malignant lymphoma; acute leukaemia; chronic hepatic obstruction;
KW kidney failure; surgical trauma; transfusion trauma; infection;
KW snakebite; haemorrhagic uraemia; splenomegaly; Barnard-Soulier disease;
KW Glanzmann's thrombasthenia; idiopathic thrombocytopenic purpura; human.
XX
OS Homo sapiens.
XX
FN WO2003057241-A1.
XX
PD 17-JUL-2003.
XX
PF 27-DEC-2002; 2002WO-JP013862.
XX
PR 28-DEC-2001; 2001JP-00400330.
XX
PA (DAIL-) DAILCHI SUNTORY PHARMA CO LTD.
PA (SUNR) SUNTORY LTD.
PA (DAIL-) DAILCHI SUNTORY BIOMEDICAL RES LTD.
XX
PI Miura K, Haruyama M, Kodama S;
XX
DR WPI; 2003-587077/55.
DR N-PSDB; ADA37013.
XX
PT Agents containing cofillin promoting proliferation and differentiation of
PT haematopoietic stem cells and their precursors for treatment of
PT haematopoietic deficiency diseases.
XX
PS Claim 2; Fig 1; 57pp; Japanese.
XX

CC The present invention describes agents (A) promoting the proliferation
CC and/or differentiation of haematopoietic stem cells and/or their
CC precursor cells. (A) contain cofillin or a peptide of similar activity as
CC active component. Also described: (1) promoting the proliferation and/or
CC differentiation of haematopoietic stem cells and/or their precursor
CC cells, using (A); and (2) treating diseases associated with
CC haematopoietic cell deficiency, using (A). (A) have vasotropic,
CC antianaemic, cytostatic, vulnerable, nephrotropic and hepatotropic
CC activities. (A) can be used for treating and preventing diseases

CC associated with a diffuse decrease in haematopoietic cell numbers and/or
CC haematopoietic hypofunction, such as Fanconi's disease, malignant
CC lymphoma, acute leukaemia, chronic hepatic obstruction, kidney failure,
CC surgical or transfusion trauma, serious infections, snakebite,
CC haemorrhagic uraemia, splenomegaly, Barnard-Soulier disease, Glanzmann's
CC thrombasthenia, and idiopathic thrombocytopenic purpura. The present
CC sequence represents human cofillin, which is given in the 'embodiment
CC of the present invention.
XX
SQ Sequence 166 AA;
Query Match 100.0%; Score 846; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSEDKKNIIIEGKEILVGDV 60
Db 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSEDKKNIIIEGKEILVGDV 60
Qy 61 GOTVDDPYATFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMIYASS 120
Db 61 GOTVDDPYATFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMIYASS 120
Qy 121 KDAIKKKLTGKHELOQANCYEEVKDRCTLAELGSSAVISLEGKPL 166
Db 121 KDAIKKKLTGKHELOQANCYEEVKDRCTLAELGSSAVISLEGKPL 166

RESULT 3
ADI24535
ID ADI24535 standard; protein; 166 AA.
XX
AC ADI24535;
XX
DT 15-APR-2004 (first entry)
XX
DE Human modifier of Chk1 (MCHK) protein SEQ ID NO:85.
XX
KW Chk1 pathway modulating agent; modifier of Chk1; MCHK; cytostatic;
KW Gene therapy; cancer; human.
XX
OS Homo sapiens.
XX
FN WO2004004785-A1.
XX
PD 15-JAN-2004.
XX
PF 09-JUL-2003; 2003WO-US021379.
XX
PR 10-JUL-2002; 2002US-0394845P.
PR 16-SEP-2002; 2002US-0410986P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Francis-Lang H, Roche S, Joo DM, Nicoll M, Hai B, Zhang H;
PI Lickteig K, Amundsen CD, Jin Y, Adamkiewicz JI, Platt DM;
PI Hammonds RG;
XX
DR WPI; 2004-083465/08.
DR N-PSDB; ADI24485.
XX
PT Identifying a candidate Chk1 pathway modulating agent for treating e.g.,
PT cancer, comprises contacting an assay system comprising a MCHK
PT polypeptide or nucleic acid with a test agent and detecting a test agent-
PT biased activity.
XX
PS Example; SEQ ID NO 85; 266pp; English.
XX

CC The present invention describes a method for identifying a candidate Chk1
CC pathway modulating agent. The method comprises: (a) providing an assay
CC system comprising a modifier of Chk1 (MCHK) polypeptide or nucleic acid;
CC (b) contacting the system with a test agent, where the system provides a
CC reference activity except in the presence of the test agent; and (c)

CC detecting a test agent-biased activity, and a difference between the test
 CC agent-biased activity and the reference activity. Also described: (1) a
 CC method for modulating Chk1 pathway of a cell; (2) a method for modulating
 CC Chk1 pathway in a mammalian cell; and (3) a method for diagnosing a
 CC disease in a patient. A MCHK sequence has cytostatic activity, and can be
 CC used in gene therapy. The method is useful for identifying a candidate
 CC Chk1 pathway-modulating agent for preparing a composition for diagnosing
 CC or treating e.g., cancer. The present sequence represents a human MCHK
 CC protein, which is used in the exemplification of the present invention.

XX SQ Sequence 166 AA;
 Query Match 100.0%; Score 846; DB 8; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.4e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASGVAVSDGVTKVFNDDMKVRKSSSTPEEVKKRKAFLFCLSEDKNIIIEEGKEILLVGDV 60
 DB 1 MASGVAVSDGVTKVFNDDMKVRKSSSTPEEVKKRKAFLFCLSEDKNIIIEEGKEILLVGDV 60
 QY 61 GOTVDDPYATFVKMLPDKDCRYALYDATYETKESKEDLVFIFWAPESAPLSKMIYASS 120
 DB 61 GOTVDDPYATFVKMLPDKDCRYALYDATYETKESKEDLVFIFWAPESAPLSKMIYASS 120
 QY 121 KDAIKKLTGIRKHELQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166
 DB 121 KDAIKKLTGIRKHELQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166

RESULT 4
 ADO05889
 ID ADO05889 standard; protein; 166 AA.
 AC ADO05889;
 DT 15-JUL-2004 (first entry)
 XX Human cofillin polypeptide.
 DE Cofillin; inflammatory disease; antiasthmatic; human.
 KW Cofillin; inflammatory disease; antiasthmatic; human.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO2004035092-A2.
 XX 29-APR-2004.
 XX 15-OCT-2003; 2003WO-GB004450.
 XX 15-OCT-2002; 2002GB-00024014.
 PR (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA (FARB) BAYER HEALTHCARE AG.
 XX Bacon KB, Herrath HMAG, Liu N, Rohlf C;
 DR WPI; 2004-348336/32.
 DR N-PSDB; ADO05890.
 XX Treating or preventing an inflammatory disease, e.g., asthma comprises
 PT administering to a subject an agonist or antagonist of cofillin isoform 1
 PT or 2 that modulates the expression or activity of a cofillin polypeptide.
 XX Claim 6; SEQ ID NO 1; 47pp; English.
 PS The invention relates to treating or preventing an inflammatory disease
 CC and involves administering to a subject, an agent that modulates the
 CC expression or activity of a cofillin polypeptide. The agent is an agonist
 CC or antagonist of cofillin isoform 1 or 2. Antiasthmatic. The method is
 CC useful in treating or preventing an inflammatory disease, e.g., asthma.
 CC The present sequence represents a human cofillin polypeptide.
 XX Sequence 166 AA;
 XX

Query Match 100.0%; Score 846; DB 8; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.4e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASGVAVSDGVTKVFNDDMKVRKSSSTPEEVKKRKAFLFCLSEDKNIIIEEGKEILLVGDV 60
 DB 1 MASGVAVSDGVTKVFNDDMKVRKSSSTPEEVKKRKAFLFCLSEDKNIIIEEGKEILLVGDV 60
 QY 61 GOTVDDPYATFVKMLPDKDCRYALYDATYETKESKEDLVFIFWAPESAPLSKMIYASS 120
 DB 61 GOTVDDPYATFVKMLPDKDCRYALYDATYETKESKEDLVFIFWAPESAPLSKMIYASS 120
 QY 121 KDAIKKLTGIRKHELQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166
 DB 121 KDAIKKLTGIRKHELQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166
 RESULT 5
 ADO30534
 ID ADO30534 standard; protein; 166 AA.
 AC ADO30534;
 DT 23-SEP-2004 (first entry)
 XX Pancreas cancer marker - non-muscle cofillin isoform.
 DE Cytostatic; diagnosis; pancreatic cancer; antibody; antisense construct;
 KW differential expression.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO2004055519-A2.
 XX 01-JUL-2004.
 PD 11-DEC-2003; 2003WO-EP014057.
 PF 17-DEC-2002; 2002EP-00028058.
 PR 05-NOV-2003; 2003EP-00025237.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.
 XX Chen J, Hu L, Liu TH, Lu ZH, Shen Y;
 XX WPI; 2004-488121/46.
 DR New specific markers comprises at least one polypeptide up-regulated in
 PT pancreatic cancer, useful for diagnosing pancreatic cancer.
 XX Claim 1; SEQ ID NO 21; 381pp; English.
 XX The invention relates to a marker (I) for diagnosis of pancreatic cancer
 CC comprising at least one polypeptide selected from 55 proteins up-
 CC regulated in pancreatic cancer (Table 2 and Table 3, given in the
 CC specification) or from 68 proteins with higher levels in pancreatic
 CC cancer compared to normal tissue (Table 6, given in the specification).
 CC (I) is a polypeptide for use as a marker or as a component of a marker
 CC for diagnosis of pancreatic cancer and/or the susceptibility to
 CC pancreatic cancer. A compound (antibody, an antibody-derivative, an
 CC antibody fragment, a peptide, or an antisense construct) identified by
 CC screening methods using (I) is useful for treatment or prevention of
 CC pancreatic cancer. It is also useful for the preparation of a diagnostic
 CC composition for diagnosing pancreatic cancer or a predisposition for
 CC pancreatic cancer. The current polypeptides were found to be
 CC differentially expressed in pancreatic tissue obtained from individuals
 CC suffering from pancreatic cancer as compared to healthy pancreatic
 CC tissue. They have been identified as suitable as markers of pancreatic
 CC cancer for early diagnosis of the disease. This sequence corresponds to a
 CC protein marker of the invention.
 XX

SQ Sequence 166 AA;
 Query Match 100.0%; Score 846; DB 8; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.4e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGVAVSDGVIKVFNDMKVRKSTPEEVKKRKAVALFCLSEDKNNILLEGKILVGDV 60
 DB 64 MASGVAVSDGVIKVFNDMKVRKSTPEEVKKRKAVALFCLSEDKNNILLEGKILVGDV 123
 QY 61 GQTVDDPYATFVKMLPKDKCRYALYDATYETKESKEDLVFIWAPESAPLKSMIYASS 120
 DB 124 GQTVDDPYATFVKMLPKDKCRYALYDATYETKESKEDLVFIWAPESAPLKSMIYASS 183
 QY 121 KDAIKKKLTGKIKHELOANCYEEVKDRCTLAELGSGSAVISLEGKPL 166
 DB 184 KDAIKKKLTGKIKHELOANCYEEVKDRCTLAELGSGSAVISLEGKPL 229

RESULT 7
 ABR41637
 ID ABR41637 standard; protein; 187 AA.
 XX
 AC ABR41637;
 DT 02-JUN-2003 (first entry)
 XX
 DE Human DITHP cytoskeletal protein.
 XX
 KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
 KW cancer; cell proliferative disorder; autoimmune disorder;
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 KW neurological disorder; gastrointestinal disorder; transport disorder;
 KW connective tissue disorder; drug screening; proteomic analysis;
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
 KW disease model; toxicological testing; transcript imaging;
 KW cytoskeletal protein.
 XX
 OS Homo sapiens.
 OS XX
 PN WO200297031-A2.
 PN XX
 PD 05-DEC-2002.
 PD XX
 PF 27-MAR-2002; 2002WO-US010056.
 PF XX
 PR 28-MAR-2001; 2001US-0279619P.
 PR XX
 PR 29-MAR-2001; 2001US-0280067P.
 PR XX
 PR 29-MAR-2001; 2001US-0280068P.
 PR XX
 PR 16-MAY-2001; 2001US-0291280P.
 PR XX
 PR 17-MAY-2001; 2001US-0291829P.
 PR XX
 PR 19-MAY-2001; 2001US-0291849P.
 PR XX
 PR 19-JUN-2001; 2001US-0299428P.
 PR XX
 PR 20-JUN-2001; 2001US-0299776P.
 PR XX
 PR 20-JUN-2001; 2001US-0300001P.
 PR XX
 PA (INCY-) INCYTE GENOMICS INC.
 PA XX
 XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Ameshey SR;
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
 PI Peralta CH, David MH, Lewis SA, Chen AU, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RV, Urashka ME;
 XX WPI; 2003-129518/12.
 DR N-PSDB; ACC46574.
 DR XX
 XX Novel human diagnostic and therapeutic polypeptide useful for identifying
 PT test compound which specifically binds to a polypeptide encoded by human
 PT diagnostic and therapeutic polynucleotide, and to induce antibodies.
 XX
 PS Claim 27; SEQ ID NO 1172; 591pp; English.
 PS XX
 CC The invention relates to novel human diagnostic and therapeutic
 CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
 CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to
 CC polynucleotide sequences at least 90% identical to the dithp cDNA
 CC sequences of the invention; recombinant vectors, host cells and

SQ Sequence 229 AA;
 Query Match 100.0%; Score 846; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 2.2e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGVAVSDGVIKVFNDMKVRKSTPEEVKKRKAVALFCLSEDKNNILLEGKILVGDV 60
 DB 1 MASGVAVSDGVIKVFNDMKVRKSTPEEVKKRKAVALFCLSEDKNNILLEGKILVGDV 60
 QY 61 GQTVDDPYATFVKMLPKDKCRYALYDATYETKESKEDLVFIWAPESAPLKSMIYASS 120
 DB 61 GQTVDDPYATFVKMLPKDKCRYALYDATYETKESKEDLVFIWAPESAPLKSMIYASS 120
 QY 121 KDAIKKKLTGKIKHELOANCYEEVKDRCTLAELGSGSAVISLEGKPL 166
 DB 121 KDAIKKKLTGKIKHELOANCYEEVKDRCTLAELGSGSAVISLEGKPL 166

RESULT 6
 ADQ65133
 ID ADQ65133 standard; protein; 229 AA.
 XX
 AC ADQ65133;
 DT 07-OCT-2004 (first entry)
 XX
 DE Novel human protein sequence #106.
 DE XX
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KW gene therapy; diagnostic marker; morbid state; osteoporosis;
 KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
 KW cancer.
 XX
 OS Homo sapiens.
 OS XX
 PN EPI440981-A2.
 PN XX
 PD 28-JUL-2004.
 PD XX
 PF 21-JAN-2004; 2004EP-00001196.
 PF XX
 PR 21-JAN-2003; 2003JP-00102206.
 PR XX
 PR 09-MAY-2003; 2003JP-00131392.
 PR XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 PA XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Nagai K, Irie R;
 XX WPI; 2004-535376/52.
 DR N-PSDB; ADQ62945.
 DR XX
 XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 PT XX
 PS Claim 1; SEQ ID NO 2294; 2449pp; English.
 PS XX
 XX The invention relates to 2495 novel polynucleotides (I) and their encoded
 CC polypeptides, sequences hybridizing to these nucleotides, sequences
 CC encoding partial polypeptides and sequences having 70% or 90% identity to
 CC the nucleotide and protein sequences. The nucleotides and polypeptides
 CC are useful as diagnostic markers or therapeutic target for the diseases
 CC or morbid states. They are also useful for treating osteoporosis,
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
 CC dementia and various cancers. This sequence corresponds to a protein
 CC sequence of the invention.
 CC XX

transgenic organisms comprising a dithp nucleic acid sequence; the recombinant production of DTHP proteins; antibodies specific for DTHP proteins; microarrays comprising dithp nucleic acid sequences; methods of detecting dithp nucleotide and protein sequences; methods of screening for compounds which specifically bind a DTHP protein; and methods of assessing the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DTHP proteins may be used in the diagnosis of a wide variety of conditions including cancer and other cell proliferative disorders; autoimmune or inflammatory disorders; bacterial, viral, fungal or parasitic infections; hormonal disorders; metabolic disorders; neurological disorders; gastrointestinal disorders; transport disorders; and connective tissue disorders. They may also be used to screen for modulators of protein activity or gene expression. DTHP proteins can additionally be used in analysis of the proteome of a tissue or cell type and to induce antibodies. The dithp nucleic acids are additionally useful in somatic or germline gene therapy of the disorders mentioned above, as a source of antisense sequences, as a source of probes and primers, in genotyping and identification of individuals, in the generation of transgenic animal models of human disease or knock in humanised animals, in toxicological testing, and in transcript imaging. The present sequence represents a DTHP protein which is a cytoskeletal protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 99.5%; Score 842; DB 6; Length 187;
Best Local Similarity 99.4%; Pred. No. 4.5e-83;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASGAVSDGVIVKFNMDKVRKSTPEEVKKRKAFLFCLSEDKNIIILEGKEILVGDV 60
DB 22 MASGAVSDGVIVKFNMDKVRKSTPEEVKKRKAFLFCLSEDKNIIILEGKEILVGDV 81
QY 61 GQTVDDPYATFVKMLPKDCRYALDYATYETKESKEDLVFIWAPESAPLKSXMIYASS 120
DB 82 GQTVDDPYATFVKMLPKDCRYALDYATYETKESKEDLVFIWAPESAPLKSXMIYASS 141
QY 121 KDAIKKLLTGIKHQLQANCVVEVKDRCTLAELKGGSAVLSLEGKPL 166
DB 142 KDAIKKLLTGIKHQLQANCVVEVKDRCTLAELKGGSAVLSLEGKPL 187

RESULT 8
ADN99790
ID ADN99790 standard; protein; 239 AA.
AC ADN99790;
DT 29-JUL-2004 (first entry)
DE Novel human protein sequence #606.
XX anti-inflammatory; dermatological; neuroprotective; immunomodulator;
KW antibacterial; virucide; antiparasitic; cytostatic; gene therapy;
KW vaccine; inflammatory; CNS; immune disorder; cancer; psoriasis; diabetes;
KW early aging; hormonal imbalance; ischemic heart disease;
KW ulcerative colitis.
XX Homo sapiens.
XX WO2004038003-A2.
XX 06-MAY-2004.
XX 24-OCT-2003; 2003WO-US033947.
XX 25-OCT-2002; 2002US-0421061P.
XX 25-OCT-2002; 2002US-0421080P.
XX 25-OCT-2002; 2002US-0421552P.
XX 25-OCT-2002; 2002US-0421614P.
XX 30-OCT-2002; 2002US-0422177P.

transgenic organisms comprising a dithp nucleic acid sequence; the recombinant production of DTHP proteins; antibodies specific for DTHP proteins; microarrays comprising dithp nucleic acid sequences; methods of detecting dithp nucleotide and protein sequences; methods of screening for compounds which specifically bind a DTHP protein; and methods of assessing the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DTHP proteins may be used in the diagnosis of a wide variety of conditions including cancer and other cell proliferative disorders; autoimmune or inflammatory disorders; bacterial, viral, fungal or parasitic infections; hormonal disorders; metabolic disorders; neurological disorders; gastrointestinal disorders; transport disorders; and connective tissue disorders. They may also be used to screen for modulators of protein activity or gene expression. DTHP proteins can additionally be used in analysis of the proteome of a tissue or cell type and to induce antibodies. The dithp nucleic acids are additionally useful in somatic or germline gene therapy of the disorders mentioned above, as a source of antisense sequences, as a source of probes and primers, in genotyping and identification of individuals, in the generation of transgenic animal models of human disease or knock in humanised animals, in toxicological testing, and in transcript imaging. The present sequence represents a DTHP protein which is a cytoskeletal protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

PR 10-OCT-2002; 2002US-0422178P.
PR 15-NOV-2002; 2002US-0426355P.
PR 15-NOV-2002; 2002US-0426384P.
PR 15-NOV-2002; 2002US-0426394P.
PR 15-NOV-2002; 2002US-0426430P.
PR 15-NOV-2002; 2002US-0426916P.
PR 27-NOV-2002; 2002US-0429224P.
PR 27-NOV-2002; 2002US-0429275P.
PR 27-NOV-2002; 2002US-0429302P.
PR 27-NOV-2002; 2002US-0429326P.
PR 27-NOV-2002; 2002US-0429651P.
PR 04-DEC-2002; 2002US-0430645P.
PR 04-DEC-2002; 2002US-0430651P.
PR 04-DEC-2002; 2002US-0430657P.
PR 04-DEC-2002; 2002US-0430663P.
PR 04-DEC-2002; 2002US-0430668P.
PR 04-DEC-2002; 2002US-0430684P.
PR 05-DEC-2002; 2002US-0430937P.
PR 05-DEC-2002; 2002US-0430965P.
PR 05-DEC-2002; 2002US-0431458P.
PR 12-DEC-2002; 2002US-0433251P.
PR 12-DEC-2002; 2002US-0433500P.
PR 13-DEC-2002; 2002US-0433316P.
PR 13-DEC-2002; 2002US-0433318P.
PR 23-DEC-2002; 2002US-0436236P.
PR 03-JAN-2003; 2003US-0437914P.
PR 17-JAN-2003; 2003US-0440820P.
PR 18-APR-2003; 2003US-0463700P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.
PR 02-MAY-2003; 2003US-0467132P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 22-MAY-2003; 2003US-0471336P.
PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-047609P.
PR 09-JUN-2003; 2003US-0476621P.
PR 09-JUN-2003; 2003US-0476632P.
PR 08-JUL-2003; 2003US-0485217P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485325P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenback RF, Kothakota S, Lin H, Linnemann T, Pierce K, Wang Y;
PI Wong JGP, Wu G, Zhang H, Zeng C;
XX WPI; 2004-365511/34.
XX N-PSDB; ADN99006.
XX New nucleic acid molecules, useful in preparing a composition for treating or preventing e.g. inflammatory, CNS, bacterial or viral disorders, cancer, psoriasis, diabetes, ischemic heart disease or ulcerative colitis.

PS Claim 14; SEQ ID NO 1390; 532pp; English.

XX This invention relates to a nucleic acid molecule comprising a

CC polynucleotide sequence or its complement that encodes a polypeptide. The

CC nucleic acid is useful in preparing a composition for treating or

CC preventing inflammatory, CNS, immune, bacterial or viral disorder,

CC cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic

CC heart disease or ulcerative colitis. This sequence corresponds to a

CC protein of the invention.

XX

SQ Sequence 239 AA;

Query Match 99.4%; Score 841; DB 8; Length 239;

Best Local Similarity 100.0%; Pred. No. 8.2e-83;

Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASGVASDGVIVFNDMKVRKSTPEEVKRRKKAFLFCLSEDKNIIIEGKEILVGDVG 61

Db 75 ASGVASDGVIVFNDMKVRKSTPEEVKRRKKAFLFCLSEDKNIIIEGKEILVGDVG 134

Qy 62 QTVDPPYATFVKMLPDKCRYALDYATYETKESKEDLVFIWAPESAPLKSKMIYASSK 121

Db 135 QTVDPPYATFVKMLPDKCRYALDYATYETKESKEDLVFIWAPESAPLKSKMIYASSK 194

Qy 122 DAIKKLTGKHQELQANCYBEVKDRCCTLAELGGSAVISLEGKPL 166

Db 195 DAIKKLTGKHQELQANCYBEVKDRCCTLAELGGSAVISLEGKPL 239

RESULT 9

ADJ70464

ID ADJ70464 standard; protein; 149 AA.

XX

AC ADJ70464;

XX

XX 06-MAY-2004 (first entry)

XX Human heat mitochondrial protein as a therapeutic target SeqID2270.

XX mitochondrial; human; screening assay; diabetes mellitus;

XX Huntington's disease; osteoarthritis;

XX Leber's hereditary optic neuropathy; LHON;

XX mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

XX myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

XX neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;

XX osteopathic; ophthalmological; cytostatic.

XX

OS Homo sapiens.

XX

XX WO2003087768-A2.

XX

PD 23-OCT-2003.

XX

XX 04-APR-2003; 2003WO-US010870.

XX

XX 12-APR-2002; 2002US-0372843P.

XX

PR 17-JUN-2002; 2002US-0389987P.

XX

PR 20-SEP-2002; 2002US-0412418P.

XX

XX (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.

PA

XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

PI Warnock DE;

PI

XX WPI; 2003-845369/78.

DR

XX Identifying a mitochondrial target for drug screening assays and for

PT treating diseases associated with altered mitochondrial function,

PT comprises detecting a modified polypeptide in a sample and correlating

PT with the disease.

XX

XX Claim 1; SEQ ID NO 2270; 180pp; English.

PS

XX This invention relates to novel mitochondrial targets that can be used

CC for therapeutic intervention in treating a disease associated with

CC altered mitochondrial function. Specifically, it refers to a method for

CC identifying proteins of the human heart mitochondrial proteome that are

CC useful for drug screening assays, as well as therapeutic targets. The

CC present invention describes a method for identifying such proteins that

CC can be used in the treatment of various diseases associated with altered

CC mitochondrial function including diabetes mellitus, Huntington's disease,

CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial

CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy

CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these

CC compositions have neuroprotective, nontropic, antidiabetic,

CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and

CC cytostatic activities. This polypeptide sequence is a human heart

CC mitochondrial protein of the invention.

XX

SQ Sequence 149 AA;

Query Match 90.3%; Score 764; DB 7; Length 149;

Best Local Similarity 100.0%; Pred. No. 1e-74;

Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MKVRKSTPEEVKRRKKAFLFCLSEDKNIIIEGKEILVGDVGQTVDDPYATFVKMLPD 77

Db 1 MKVRKSTPEEVKRRKKAFLFCLSEDKNIIIEGKEILVGDVGQTVDDPYATFVKMLPD 60

Qy 78 KCRYALDYATYETKESKEDLVFIWAPESAPLKSKMIYASSKDAIKKLTGKHQELQ 137

Db 61 KCRYALDYATYETKESKEDLVFIWAPESAPLKSKMIYASSKDAIKKLTGKHQELQ 120

Qy 138 NCYEEVKDRCCTLAELGGSAVISLEGKPL 166

Db 121 NCYEEVKDRCCTLAELGGSAVISLEGKPL 149

RESULT 10

ABR41956

ID ABR41956 standard; protein; 166 AA.

XX

XX ABR41956;

XX

DT 11-AUG-2003 (first entry)

XX

DE Mouse cofillin, implicated in pain.

XX

XX Mouse; cofillin; nociceptive; analgesic; signal transduction;

XX transgenic animal.

XX

XX Mus musculus.

XX

XX EP1281775-A2.

PN

XX

XX 05-FEB-2003.

PD

XX

XX 26-JUL-2002; 2002EP-00255231.

PF

XX

XX 27-JUL-2001; 2001GB-00018354.

PR

XX

XX 07-FEB-2002; 2002GB-00002892.

PR

XX

XX (WARN) WARNER LAMBERT CO.

PA

XX Brooksbank RA, Dixon AK, Lee K, Pinnock RD;

PI

XX WPI; 2003-335009/32.

DR

XX N-PSDB; ACC48821.

DR

XX Use of isolated gene or nucleic acid sequence, recombinant vector, host

PT cell, non-human animal, polypeptide encoded by the nucleic acid sequence,

PT or antibody, for screening of compounds for the treatment of pain, or for

PT diagnosing pain.

XX

XX Disclosure; Page 65-66; 87pp; English.

PS

XX The present sequence is the protein sequence of mouse cofillin. This is
CC encoded by a gene that has been identified as being up-regulated in 2
CC models of chronic pain, i.e. streptozocin-induced diabetes and chronic
CC constrictive injury to a nerve leading to the spine. The expression
CC products of such genes can be used to screen libraries for compounds and
CC peptide agonists and antagonists of gene product activity that may be
CC useful in the treatment or prevention of chronic pain, and in the
CC development of diagnostic tools for the identification and
CC characterisation of pain
XX
SQ Sequence 166 AA;

Query Match 83.0%; Score 702; DB 6; Length 166;
Best Local Similarity 81.3%; Pred. No. 6.6e-68;
Matches 135; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

QY 1 MASGVAVSDGVIVKVFNDKVKRSTPEEVKKRKAFLFCLSEDKNIIIEEGKEIIVGDV 60
Db 1 MASGVTVNDEVIVKVFNDKVKRSTQEEIKRKAFLFCLSDDDKROIIVEEAKQIIVGDI 60

QY 61 GQTVDDPYATFVKMLPDKCRYALYDATYETKESKKEDLVFIWAPESAPLKSMMIYASS 120
Db 61 GDTVEDPYTSFVKLLPLNDCRYALYDATYETKESKKEDLVFIWAPESAPLKSMMIYASS 120

QY 121 KDAIKKKLTGIRKHELQANCYEEVKDRTLAELKGGSAVISLECKPL 166
Db 121 KDAIKKKFTGIRKHEWQVNGLLDDIKDRSTLGEKLGGSVWVSLGKPL 166

RESULT 11
AAW78545
ID AAW78545 standard; protein; 166 AA.
XX
AC AAW78545;
XX
DT 06-NOV-2001 (first entry)
DE Human protein SEQ ID NO 1207.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
XX Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX
XX 27-APR-2000; 2000US-00560875.
XX
XX 20-JUN-2000; 2000US-00598075.
XX
XX 19-JUL-2000; 2000US-00620325.
XX
XX 01-SEP-2000; 2000US-00654936.
XX
XX 15-SEP-2000; 2000US-00663561.
XX
XX 20-OCT-2000; 2000US-00693325.
XX
XX 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
DR N-PSDB: AAK51678.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.

XX Claim 20; Page 3461-3462; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 166 AA;

Query Match 82.6%; Score 699; DB 4; Length 166;
Best Local Similarity 80.7%; Pred. No. 1.4e-67;
Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 MASGVAVSDGVIVKVFNDKVKRSTPEEVKKRKAFLFCLSEDKNIIIEEGKEIIVGDV 60
Db 1 MASGVTVNDEVIVKVFNDKVKRSTQEEIKRKAFLFCLSDDDKROIIVEEAKQIIVGDI 60

QY 61 GQTVDDPYATFVKMLPDKCRYALYDATYETKESKKEDLVFIWAPESAPLKSMMIYASS 120
Db 61 GDTVEDPYTSFVKLLPLNDCRYALYDATYETKESKKEDLVFIWAPESAPLKSMMIYASS 120

QY 121 KDAIKKKLTGIRKHELQANCYEEVKDRTLAELKGGSAVISLECKPL 166
Db 121 KDAIKKKFTGIRKHEWQVNGLLDDIKDRSTLGEKLGGSVWVSLGKPL 166

RESULT 12
ADB75248
ID ADB75248 standard; protein; 166 AA.
XX
AC ADB75248;
XX
DT 04-DEC-2003 (first entry)
XX
DE Prostate cancer marker protein.
XX
KW Prostate; cancer; cytostatic; gene therapy; marker.
XX
OS Homo sapiens.
XX
XX WO2003009814-A2.
XX
XX 06-FEB-2003.
XX
XX 25-JUL-2002; 2002WO-US023913.
XX
XX 25-JUL-2001; 2001US-0307982P.
XX
XX 22-AUG-2001; 2001US-0314356P.
XX
XX 25-SEP-2001; 2001US-0325020P.
XX
XX 12-DEC-2001; 2001US-0341746P.
XX
XX 05-MAR-2002; 2002US-0362158P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
PI Hoersht S, Kanatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
XX
XX WPI: 2003-248033/24.
XX
XX New nucleic acid molecule, useful for diagnosing or treating prostate
XX cancer.
XX
XX Disclosure; SEQ ID NO 72; 99pp; English.

XX The invention relates to newly discovered cancer markers associated with
 CC the cancerous state of prostate cells. Also disclosed is a method of
 CC assessing whether a patient is afflicted with prostate cancer. The method
 CC of the invention involves assessing whether a patient is afflicted with
 CC prostate cancer by comparing the level of expression of a marker in a
 CC patient sample and the normal level of expression of the marker in a
 CC control non-prostate cancer sample, where a significant increase in the
 CC level of expression of the marker in the patient sample and the normal
 CC level indicates that the patient is afflicted with prostate cancer.
 CC Nucleic acids of the invention are useful for diagnosing or treating
 CC prostate cancer, and may be useful in gene therapy. Sequences given in
 CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 166 AA;
 Query Match 82.6%; Score 699; DB 7; Length 166;
 Best Local Similarity 80.7%; Pred. No. 1.4e-67;
 Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MASGVAVSDGVIKVFNDMKVRKSTPEEVKRRKAVLFCLSDDKQRIIVEEAKQILVGDI 60
 DB 1 MASGVTVNDEVIKVFNDMKVRKSTQEEIKRRKAVLFCLSDDKQRIIVEEAKQILVGDI 60
 QY 61 GQTVDDPYATFVKMLPDKCRYALYDATYETKESKEDLVFIWAPESAPLKSKMIYASS 120
 DB 61 GDTVEDPYTSFVKLLPLNDCRYALYDATYETKESKEDLVFIWAPESAPLKSKMIYASS 120
 QY 121 KDAIKKLTGIKHELOANCYEEVKDRCCTLAELKGGSAVISLEGKPL 166
 DB 121 KDAIKKFTGIKHEWQVNGLLDIIKDRSTLGEKLGNNVVVSLGKPL 166
 RESULT 13
 ADJ70104
 ID ADJ70104 standard; protein; 166 AA.
 AC ADJ70104;
 XX
 XX 06-MAY-2004 (first entry)
 XX Human heat mitochondrial protein as a therapeutic target SeqID1910.
 XX
 KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 XX
 OS Homo sapiens.
 XX
 XX WO2003087768-A2.
 XX
 XX 23-OCT-2003.
 XX
 XX 04-APR-2003; 2003WO-US010870.
 XX
 XX 12-APR-2002; 2002US-0372843P.
 XX 17-JUN-2002; 2002US-039987P.
 XX 20-SEP-2002; 2002US-0412418P.
 XX
 XX (MITO-) MITOKOR.
 XX (BUCK-) BUCK INST AGE RES.
 XX
 XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 XX Warnock DE;
 XX WPI; 2003-845369/78.

XX Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX
 PS Claim 1; SEQ ID NO 1910; 180pp; English.
 CC
 CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 XX
 SQ Sequence 166 AA;
 Query Match 82.6%; Score 699; DB 7; Length 166;
 Best Local Similarity 80.7%; Pred. No. 1.4e-67;
 Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MASGVAVSDGVIKVFNDMKVRKSTPEEVKRRKAVLFCLSDDKQRIIVEEAKQILVGDI 60
 DB 1 MASGVTVNDEVIKVFNDMKVRKSTQEEIKRRKAVLFCLSDDKQRIIVEEAKQILVGDI 60
 QY 61 GQTVDDPYATFVKMLPDKCRYALYDATYETKESKEDLVFIWAPESAPLKSKMIYASS 120
 DB 61 GDTVEDPYTSFVKLLPLNDCRYALYDATYETKESKEDLVFIWAPESAPLKSKMIYASS 120
 QY 121 KDAIKKLTGIKHELOANCYEEVKDRCCTLAELKGGSAVISLEGKPL 166
 DB 121 KDAIKKFTGIKHEWQVNGLLDIIKDRSTLGEKLGNNVVVSLGKPL 166
 RESULT 14
 ADI24536
 ID ADI24536 standard; protein; 166 AA.
 XX
 AC ADI24536;
 XX
 XX 15-APR-2004 (first entry)
 XX Human modifier of Chk1 (MCHK) protein SEQ ID NO:86.
 XX
 DE Chk1 pathway modulating agent; modifier of Chk1; MCHK; cytostatic;
 XX gene therapy; cancer; human.
 KW
 KW Homo sapiens.
 XX
 OS
 XX WO2004004785-A1.
 XX
 XX 15-JAN-2004.
 XX
 XX 09-JUL-2003; 2003WO-US021379.
 XX
 XX 10-JUL-2002; 2002US-0394845P.
 XX 16-SEP-2002; 2002US-0410986P.
 XX
 XX (EXEL-) EXELIXIS INC.
 XX
 XX Francis-Lang H, Roche S, Joo DM, Nicoll M, Hai B, Zhang H;
 XX Lickteig K, Amundsen CD, Jin Y, Adamkewicz JI, Platt DM;
 XX Hammonds RG;

PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241836P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-476182/51.

N-PSDB; AAS29808.

Novel isolated human cytoskeletal element-related polypeptide useful for

PT diagnosis/treatment of neoplastic disorders, disorders associated with
 XX neural transmission, chromosomal abnormalities, autoimmune disorders.
 PS Claim 11; SEQ ID NO 93; 505pp; English.
 XX Sequences AAU18508-AAU18551 represent the cytoskeletal element-related
 CC polypeptides of the invention. Cytoskeletal polypeptides and their
 CC associated polynucleotides are useful in the diagnosis, treatment and
 CC prevention of various types of disorders in e.g. humans, mice, rabbits,
 CC goats, horses, cats, dogs, chickens or sheep. A pathological condition
 CC can be determined by determining the presence or absence of a mutation in
 CC a cytoskeletal polynucleotide. The treatable disorders include autoimmune
 CC diseases such as rheumatoid arthritis, hyperproliferative disorders such
 CC as neoplasms of the breast or liver, cardiovascular disorders such as
 CC cardiac arrest, cerebrovascular disorders such as cerebral ischaemia,
 CC nervous system disorders such as Alzheimer's disease, infections caused
 CC by bacteria, viruses and fungi, ocular disorders such as corneal
 CC infection, endocrine disorders such as premature labour and infertility,
 CC gastrointestinal disorders such as Crohn's disease, renal disorders such
 CC as glomerulonephritis and respiratory disorders such as asthma. The
 CC polypeptides can also be used to aid wound healing, to prevent skin aging
 CC due to sunburn, to maintain organs before transplantation, to regenerate
 CC tissues and in chemotaxis. The polypeptides can also be used as a food
 CC additive or preservative to increase or decrease storage capabilities.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

Query Match 82.6%; Score 699; DB 4; Length 205;

Best Local Similarity 80.7%; Pred. No. 1.9e-67;

Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVIKVNNDMKVRKSTPEEVKKKAVLFCLSDKKNIIIEGKEILVGDV 60

Db 40 MASGVVNDKVIKVNNDMKVRKSTQEEIKKKKAVLFCLSDKKNIIIEGKEILVGDV 99

Qy 61 GQTVDDPYATFVKMLPDKCRYALYDITYETKESKKEDLVFIWAPESAPLKSMIYASS 120

Db 100 GDTVEDPYTGFVKLLPLNDCRYALYDITYETKESKKEDLVFIWAPESAPLKSMIYASS 159

Qy 121 KDAIKKKLTGIKHELQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166

Db 160 KDAIKKKFTGIRHEWQVNGLLDKDRSTLGEKLGNNVVSLEGKPL 205

Search completed: May 13, 2005, 09:43:49

Job time : 164 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2005, 09:37:55 ; Search time 38 Seconds
(without alignments)
420.315 Million cell updates/sec

Title: US-10-649-952A-1
Perfect score: 846
Sequence: 1 MASGVAVSDGVKVFNDMKV.....CTLAEKLGGSAVISLEGRPL 166
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	846	100.0	166	S12632	cofilin - human
2	842	99.5	166	S49101	cofilin - rat
3	841	99.4	166	S12640	cofilin - pig
4	839	99.2	166	S12584	cofilin - mouse
5	702	83.0	166	A53812	cofilin, muscle -
6	701	82.9	166	B35703	cofilin - chicken
7	620.5	73.3	165	A35702	destrin - chicken
8	606.5	71.7	165	A35179	destrin - pig
9	606.5	71.7	165	A54184	destrin [validated
10	598.5	70.7	164	JE0223	destrin - rat
11	267.5	31.6	143	T43397	cofilin - yeast (S
12	254	30.0	137	T43245	probable actin-dep
13	227	26.8	139	T02914	actin-depolymmerizi
14	213	25.2	140	A86149	actin-depolymmerizi
15	208	24.6	132	G84717	actin-depolymmerizi
16	208	24.6	139	T02883	actin-depolymmerizi
17	205.5	24.3	142	S71361	actin-binding prot
18	201.5	23.8	148	A57569	twinstar protein -
19	200.5	23.7	133	T01232	actin-depolymmerizi
20	200.5	23.7	139	S30935	actin-depolymmerizi
21	195.5	23.1	130	T47540	actin-depolymmerizi
22	195	23.0	130	T05767	actin-depolymmerizi
23	192.5	22.8	139	T02882	actin-depolymmerizi
24	191	22.6	126	S30934	actin-depolymmerizi
25	190.5	22.5	130	T05788	actin-depolymmerizi
26	187	22.1	132	B84543	actin-depolymmerizi
27	185.5	21.9	135	T49327	cofilin related pr
28	176.5	20.9	58	A56448	destrin-like prote
29	158.5	18.7	133	T47539	actin depolymmerizi

30	157.5	18.6	49	2	B56448	cofilin-like prote
31	150.5	17.8	165	2	S41728	actin depolymmerizi
32	149.5	17.7	293	2	T33952	actin depolymmerizi
33	130	15.4	152	2	S41727	unc-60 protein - C
34	120	14.2	350	2	A55922	tyrosine kinase A6
35	104	12.3	349	2	T46362	probable tyrosine
36	98.5	11.6	358	2	T13017	hypothetical prote
37	98	11.6	328	2	T40910	probable tyrosine
38	96.5	11.4	142	1	PT0410	glia maturation fa
39	96	11.3	141	1	JDB08	glia maturation fa
40	94	11.1	141	1	S22149	glia maturation fa
41	94	11.1	390	2	H64603	probable aspartate
42	86.5	10.2	350	2	T05589	hypothetical prote
43	86.5	10.2	418	2	E64100	probable Atp-depen
44	85.5	10.1	415	2	T34156	hypothetical prote
45	85.5	10.1	509	2	T29291	hypothetical prote

ALIGNMENTS

RESULT 1

S12632
cofilin - human
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: S12632
R:Ogawa, K.; Tashima, M.; Yumoto, Y.; Okuda, T.; Sawada, H.; Okuma, M.; Maruyama, Y.
Nucleic Acids Res. 18, 7169, 1990
A:Title: Coding sequence of human placenta Cofilin cDNA.
A:Reference number: S12632; MUID:91088330; PMID:2263493
A:Accession: S12632
A:Molecule type: mRNA
A:Residues: 1-166 <OGA>
A:Cross-references: UNIPROT:P23528; EMBL:D00682; NID:G219544; PIDN:BA00589.1; PID:G21954
C:Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a pr
C:Genetics:
A:Gene: GDB:CFL1; CFL
A:Cross-references: GDB:126798; OMIM:601442
A:Map position: 11q13-11q13
C:Superfamily: cofilin
C:Keywords: actin binding; phosphoprotein
F:26-36/Region: nuclear location signal
F:104-134/Region: actin binding #status predicted

Query Match	100.0%	Score	846;	DB	1;	Length	166;
Best Local Similarity	100.0%	Pred. No.	4.8e-61;	Mismatches	0;	Indels	0;
Matches	166;	Conservative	0;				
QY	1	MASGVAVSDGVKVFNDMKVRSSTPEEVKRRKKA	VLFCLSEDKKNI	ILEEGKEILVGDV	60		
Db	1	MASGVAVSDGVKVFNDMKVRSSTPEEVKRRKKA	VLFCLSEDKKNI	ILEEGKEILVGDV	60		
QY	61	GQTVDPPATFVKMLPDKDCRYALDYATYETKESKEDLV	FWAPESAPLKS	KMIYAS	120		
Db	61	GQTVDPPATFVKMLPDKDCRYALDYATYETKESKEDLV	FWAPESAPLKS	KMIYAS	120		
QY	121	KDAIKKLTGKHKEIQANCYERVKDRTLAELKGGSAVIS	LEGGKPL	166			
Db	121	KDAIKKLTGKHKEIQANCYERVKDRTLAELKGGSAVIS	LEGGKPL	166			

RESULT 2

S49101
cofilin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Jan-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S49101; A58860; JE0222
R:Shirasawa, T.; Takahashi, H.; Sakamoto, K.; Kawashima, A.; Akashi, T.
submitted to the EMBL Data Library, October 1991
A:Description: Nucleotide sequence of rat cofilin cDNA.
A:Reference number: S49101
A:Accession: S49101

A:Molecule type: mRNA
A:Residues: 1-166 <SH>
A:Cross-references: UNIPROT:P45592; EMBL:X62908; NID:G509200; PIDN:CAA44694.1; PID:G509202
R:Shirabawa, T.
Submitted to DBJ, October 1991
A:Reference number: A58860
A:Accession: A58860
A:Molecule type: mRNA
A:Residues: 1-166 <SH2>
A:Cross-references: EMBL:X62908; NID:G509200; PIDN:CAA44694.1; PID:G509201
A:Experimental source: embryo brain
R:Kanamori, T.; Suzuki, M.M.; Titani, K.
Submitted to JIPID, August 1998
A:Description: Complete amino acid sequences and phosphorylation sites, determined by Ed
A:Reference number: JE0222
A:Accession: JE0222
A:Molecule type: protein
A:Residues: 2-166 <KAN>
C:Superfamily: cofilin
C:Keywords: acetylated amino end; phosphoprotein
F:2-166/Product: cofilin #status experimental <MAT>
F:19-34/Region: nuclear location signal
F:104-115/Region: actin binding #status predicted
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F:3/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 99.5%; Score 842; DB 2; Length 166;
Best Local Similarity 99.4%; Pred. No. 1e-60;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSEDKNIIILEGKEILVGDV 60
Db 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSEDKNIIILEGKEILVGDV 60

Qy 61 GQTVDDPYATFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASS 120
Db 61 GQTVDDPYTFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASS 120

Qy 121 KDAIKKKLTGKHELOANQCYEEVKDRCTLAELKGGSAVISLEGKPL 166
Db 121 KDAIKKKLTGKHELOANQCYEEVKDRCTLAELKGGSAVISLEGKPL 166

RESULT 3
A29240
Cofilin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 28-Aug-1989 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A29240
R:Matsumoto, S.; Yahara, I.; Yonezawa, N.; Nishida, E.; Sakai, H.
J. Biol. Chem. 263, 11564-11566, 1988
A:Title: Cloning and characterization of porcine brain cofilin cDNA. Cofilin contains th
A:Reference number: A29240; MUID:88298817; PMID:3403546
A:Accession: A29240
A:Molecule type: mRNA
A:Residues: 1-166 <MAT>
A:Cross-references: UNIPROT:P10668; GB:M20866; NID:G164424; PIDN:AAA31020.1; PID:G164425
C:Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a p
C:Superfamily: cofilin
C:Keywords: actin binding; phosphoprotein
F:26-36/Region: nuclear location signal
F:104-134/Region: actin binding #status predicted

Query Match 99.4%; Score 841; DB 1; Length 166;
Best Local Similarity 99.4%; Pred. No. 1.2e-60;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSEDKNIIILEGKEILVGDV 60
Db 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSEDKNIIILEGKEILVGDV 60

Qy 61 GQTVDDPYATFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASS 120
Db 61 GQTVDDPYTFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASS 120

Db 61 GQTVDDPYATFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASS 120

Qy 121 KDAIKKKLTGKHELOANQCYEEVKDRCTLAELKGGSAVISLEGKPL 166
Db 121 KDAIKKKLTGKHELOANQCYEEVKDRCTLAELKGGSAVISLEGKPL 166

RESULT 4
S12584
Cofilin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: S12584; JUI0201
R:Moriyama, K.; Matsumoto, S.; Nishida, E.; Sakai, H.; Yahara, I.
Nucleic Acids Res. 18, 3053, 1990
A:Title: Nucleotide sequence of mouse cofilin cDNA.
A:Reference number: S12584; MUID:90272419; PMID:2349104
A:Accession: S12584
A:Molecule type: mRNA
A:Residues: 1-166 <MOR>
A:Cross-references: UNIPROT:P18760; EMBL:D00472; NID:G220383; PIDN:BAA00364.1; PID:G2203
C:Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a p
C:Superfamily: cofilin
C:Keywords: actin binding; phosphoprotein
F:26-36/Region: nuclear location signal
F:104-134/Region: actin binding #status predicted

Query Match 99.2%; Score 839; DB 1; Length 166;
Best Local Similarity 98.8%; Pred. No. 1.7e-60;
Matches 164; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSEDKNIIILEGKEILVGDV 60
Db 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSEDKNIIILEGKEILVGDV 60

Qy 61 GQTVDDPYATFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASS 120
Db 61 GQTVDDPYTFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASS 120

Qy 121 KDAIKKKLTGKHELOANQCYEEVKDRCTLAELKGGSAVISLEGKPL 166
Db 121 KDAIKKKLTGKHELOANQCYEEVKDRCTLAELKGGSAVISLEGKPL 166

RESULT 5
A53812
Cofilin, muscle - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: A53812
R:Ono, S.; Minami, N.; Abe, H.; Obinata, T.
J. Biol. Chem. 269, 15280-15286, 1994
A:Title: Characterization of a novel cofilin isoform that is predominantly expressed in
A:Reference number: A53812; MUID:94253093; PMID:8195165
A:Accession: A53812
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-166 <ONO>
A:Cross-references: UNIPROT:P45591; GB:L29468; NID:G498016; PIDN:AAA37433.1; PID:G498017
C:Superfamily: cofilin
C:Keywords: actin binding; muscle

Query Match 83.0%; Score 702; DB 2; Length 166;
Best Local Similarity 81.3%; Pred. No. 1.8e-49;
Matches 135; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSEDKNIIILEGKEILVGDV 60
Db 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSEDKNIIILEGKEILVGDV 60

Qy 61 GQTVDDPYATFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASS 120
Db 61 GQTVDDPYTFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASS 120

J. Cell Biol. 122, 623-633, 1993

A;Title: Isolation and characterization of a regulated form of actin depolymerizing factor
A;Reference number: A40672; MUID:93328764; PMID:7687605

A;Accession: A40672

A:Molecule type: protein

A;Residues: 20-30 <MOR>

R;Agnew, B.J.; Minamide, L.S.; Bamburg, J.R.

J. Biol. Chem. 270, 17582-17587, 1995

A;Title: Reactivation of phosphorylated actin depolymerizing factor and identification of
A;Reference number: A38989; MUID:95340558; PMID:7615564

C;Contents: annotation; acetylated amino end; phosphorylation site

C;Comment: Destrin is an actin-binding protein that is capable of rapidly depolymerizing

C;Superfamily: cofilin

C;Keywords: acetylated amino end; actin binding; phosphoprotein

F;2-165/Product: destrin #status predicted <MAT>

F;26-36/Region: nuclear location signal

F;104-134/Region: actin binding #status predicted

F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

F;3/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 73.3%; Score 620.5; DB 1; Length 165;
Best Local Similarity 73.5%; Pred. No. 6.3e-43;
Matches 122; Conservative 18; Mismatches 25; Indels 1; Gaps 1;

Qy 1 MASGVAVSDGVIKVPNDMKVRKSTPEVKRKKAIVFCLSEDKKNIILEEGKEILVGVDV 60
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 1 MASGVQVADEVCRIFYDKVRKCKSTPEVKRKRKAIVFCLSPDKKCIIIVEEGKEILVGVD 60
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Qy 61 GOTVDDPYATVFVKMLPKDCKRYALYDATYETKESKKEDLVIFWAPESAPLKSKMIYASS 120
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 61 GVTVTDPFKFHVEMLPKDCKRYALYDAGFTYESKKBSELMFLWAPEQAPLKSKMIYASS 120
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Qy 121 KDAIKKKLTGIKHBLQANCYEEVDRCRTLAELKGSSAVISLEGKPL 166
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 121 KDAIKKKFKQGIEHCQANGPEDLNRAEIAEKLGGLVLVAPEGSPV 165
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 8

A35179

N:Alternate names: actin-depolymerizing factor

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 03-Aug-1990 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004

C:Accession: A35179

R;Moriyama, K.; Nishida, E.; Yonezawa, N.; Sakai, H.; Matsumoto, S.; Iida, K.; Yahara, I.
J. Biol. Chem. 265, 5768-5773, 1990

A;Title: Destrin, a mammalian actin-depolymerizing protein, is closely related to cofilin

A;Reference number: A35179; MUID:90202824; PMID:2158628

A;Accession: A35179

A:Molecule type: mRNA

A;Residues: 1-165 <MOR>

A:Cross-references: UNIPROT:P60982; GB:D90053; GB:J05290; NID:g217681; PIDN:BAAI4105.1; I

A;Experimental source: brain

C;Comment: Destrin is an actin-binding protein that is capable of rapidly depolymerizing

C;Superfamily: cofilin

C;Keywords: acetylated amino end; actin binding; phosphoprotein

F;2-165/Product: destrin #status predicted <MAT>

F;26-36/Region: nuclear location signal

F;104-134/Region: actin binding #status predicted

F;2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

F;3/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 71.7%; Score 606.5; DB 1; Length 165;
Best Local Similarity 71.1%; Pred. No. 8.4e-42;
Matches 118; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

Qy 1 MASGVAVSDGVIKVPNDMKVRKSTPEVKRKKAIVFCLSEDKKNIILEEGKEILVGVD 60
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 1 MASGVQVADEVCRIFYDKVRKCKSTPEIKRKRKAIVFCLSADKKCIIIVEEGKEILVGVD 60
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Qy 61 GOTVDDPYATVFVKMLPKDCKRYALYDATYETKESKKEDLVIFWAPESAPLKSKMIYASS 120
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 61 GVITVDPFKHFVGMKPCKCRYALYDASFTEKSRKEELMPFLWAPELAPLKSKMIYASS 120
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

A;Residues: 1-164 <KAN>
A;Cross-references: UNIPROT:Q7M0E3
C;Superfamily: cofilin
F;Keywords: acetylated amino end; phosphoprotein
F;18-33/Region: nuclear location signal
F;103-114/Region: actin binding #status predicted
F;1/Modified site: acetylated amino end (Ala) #status experimental
F;2/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 70.7%; Score 598.5; DB 2; Length 164;
Best Local Similarity 69.7%; Pred. No. 3.7e-41;
Matches 115; Conservative 24; Mismatches 25; Indels 1; Gaps 1;

QY 2 ASGVAVSDGVIKVFNDMKVRKSTPEVKRKAFLFCLSEDKNILLEGKEILVGDVG 61
||||| : : : : : ||||| : : : : : ||||| : : : : :
Db 1 ASGVQVADECRIFYDMKVRKSTPEIKKRKAIVIFCLSAADKKCIWVEEGKEILVGDVG 60
||||| : : : : : ||||| : : : : : ||||| : : : : :
QY 62 QTVDPPDYATFVKMLPKDCRYALYDATYETKSKEDLVFIWPESAPLKSMIYASSK 121
||||| : : : : : ||||| : : : : : ||||| : : : : :
Db 61 VTITDFPHFVGMPLPKDCRYALYDASFTKSRKEELMFFLWAPEQAFLKSLMIYASSK 120
||||| : : : : : ||||| : : : : : ||||| : : : : :
QY 122 DA1KKKLGTGKHLEQLANCVEEVKDRCTLAELKGSGSAVISLEGKPL 166
||||| : : : : : ||||| : : : : : ||||| : : : : :
Db 121 DA1KKKFPGLKHYYQANGPEDL-NRTSIAELKGSLIVAFEGSPV 164
||||| : : : : : ||||| : : : : : ||||| : : : : :

RESULT 11
A44397
N;Alternate names: (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 31-Dec-1993 #sequence revision 27-Jun-1994 #text change 09-Jul-2004
C;Accession: A44397; B44397; J05029; S64802; S50970; S31309; S36087
R;Moon, A.L.; Janmey, P.A.; Louie, K.A.; Drubin, D.G.
J. Cell Biol. 120, 421-435, 1993
A;Title: Cofilin is an essential component of the yeast cortical cytoskeleton.
A;Reference number: A44397; UID:93132073; PMID:8421056
A;Accession: A44397
A;Molecule type: DNA
A;Residues: 1-143 <MOO>
A;Cross-references: UNIPROT:Q03048; EMBL:Z14971; NID:g3563; PIDN:CAA78694.1; PID:g3564
A;Note: sequence extracted from NCBI backbone (NCBIN:122683, NCBI:P:122684)
A;Accession: B44397
A;Molecule type: protein
A;Residues: 43-56;83-96,'X',98;106-129,'DS',132-141 <MO2>
A;Note: sequence extracted from NCBI backbone
R;lida, K.; Moriyama, K.; Matsumoto, S.; Kawasaki, H.; Nishida, E.; Yahara, I.
Gene 124, 115-120, 1993
A;Title: Isolation of a yeast essential gene, COF1, that encodes a homologue of mammalian cofilin.
A;Reference number: JN0529; UID:93178959; PMID:8440472
A;Accession: JN0529
A;Molecule type: DNA
A;Residues: 1-143 <IID>
A;Cross-references: GB:D13230; NID:g287599; PIDN:BAA02514.1; PID:g287600
R;Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64792
A;Accession: S64802
A;Molecule type: DNA
A;Residues: 1-143 <WEH>
A;Cross-references: EMBL:Z47973; NID:g642313; PIDN:CAA88007.1; PID:g642334
A;Note: experimental source strain S288C
R;Wedler, H.; Wambutt, R.
submitted to the EMBL Data Library, January 1995
A;Description: Sequence of a 37 kb DNA fragment from chromosome XII of Saccharomyces cerevisiae.
A;Reference number: S50950
A;Accession: S50970
A;Molecule type: DNA
A;Residues: MWGKKFRSQENVKFLCS',6-143 <WEH>
A;Cross-references: EMBL:Z47973; NID:g642313; PIDN:CAA88007.1; PID:g642334
C;Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a p...
A;Genes: SGD:COF1; MIPS:YL050G

A;CROSS-references: SGD:S0003973; MIPS:YLL050C

A;Map position: 12L

A;Introns: 5/2

C;Superfamily: cofillin

C;Keywords: actin binding

F;88-118/Region: actin binding #status predicted

Query Match 31.6%; Score 267.5; DB 1; Length 143;
Best Local Similarity 37.8%; Pred. No. 1.3e-14;
Matches 54; Conservative 31; Mismatches 37; Indels 21; Gaps 3;
QY 3 SGVAVSDGVKVFNDKMKVRKSTPEEVKKRKKAVLFCLESDKKNIIIEEGKEILVGDVGQ 62
DB 4 SGVAVADESLTANDLK-----LGKKYKILFGLNDKATKTEIVVKE-----T 44
QY 63 TVDDPYATFVKMLPKDKCRYALYDATYET--KESKEDLVFIWAPESAPLKSOMIYASS 120
DB 45 STDPDYDAFLKLPENDCLYAIYDFEYINGEGKSKIVFTWSPDTPAVRSKMYVASS 104
QY 121 KDAIKKLTGKIKHELQANCVEEV 143
DB 105 KDALRRALNGVSTDVQGTDFSEV 127

RESULT 12

T43245

probable actin-depolymerizing factor - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C;Accession: T43245; T38120

R;Kawamukai, M.

submitted to the EMBL Data Library, December 1996

A;Description: S. pombe cDNA for actin depolymerizing factor.

A;Reference number: Z22362

A;Accession: T43245

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-137 <RAW>

A;CROSS-references: UNIPROT:P78929; EMBL:D89939; PIDN:BAAL4039.1

R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z21771

A;Accession: T38120

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-137 <CON>

A;CROSS-references: EMBL:Z98600; PIDN:CAB11258.1; GSPDB:GN00066; SPDB:SPAC20G4.06C

A;Experimental source: strain 972h-; cosmid C20G4

C;Genetics:

A;Gene: SPAC20G4.06C

A;Map position: 1

A;Introns: 1/3; 37/1

A;Note: adf1

C;Superfamily: cofillin

C;Keywords: actin binding

Query Match 30.0%; Score 254; DB 2; Length 137;
Best Local Similarity 35.1%; Pred. No. 1.5e-13;
Matches 53; Conservative 36; Mismatches 42; Indels 20; Gaps 3;
QY 3 SGVAVSDGVKVFNDKMKVRKSTPEEVKKRKKAVLFCLESDKKNIIIEEGKEILVGDVGQ 62
DB 4 SGVAVSPECLEAFQELKLGKS-----LRYVFKMDTKTEIVVEK-----K 44

QY 63 TVDDPYATFVKMLPKDKCRYALYDATYETKESKEDLVFIWAPESAPLKSOMIYASSKD 122

DB 45 STDKQFDFTFLGDLPEKDCRYAIYDFEFNLGEGVRNKKIIFISWPDVPIKSKMYVSSKD 104

QY 123 AIKKKLTGKIKHELQANCYBEVDRCTLAELK 153

DB 105 TLRRFTGTGTDIQTDFSEVAYE-TVLEKV 134

RESULT 13

T02914

actin-depolymerizing factor 3 - maize

C;Species: Zea mays (maize)

C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C;Accession: T02914

R;Lopez, I.; Anthony, R.G.; Maciver, S.K.; Jiang, C.J.; Khan, S.; Weeds, A.G.; Hussey, P.

Proc. Natl. Acad. Sci. U.S.A. 93, 7415-7420, 1996

A;Title: Pollen specific expression of maize genes encoding actin depolymerizing factor-1

A;Reference number: Z14757; MUID:96293540; PMID:8693008

A;Accession: T02914

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-139 <LDP>

A;CROSS-references: UNIPROT:Q41764; EMBL:X97726; NID:g1419369; PIDN:CAA66311.1; PID:g1419369

A;Experimental source: leaf

C;Genetics:

A;Gene: ASP3

C;Superfamily: cofillin

C;Keywords: actin binding

Query Match 26.8%; Score 227; DB 2; Length 139;
Best Local Similarity 36.0%; Pred. No. 2.2e-11;
Matches 54; Conservative 27; Mismatches 45; Indels 24; Gaps 5;
QY 3 SGVAVSDGVKVFNDKMKVRKSTPEEVKKRKKAVLFCLESDKKNIIIEEGKEILVGDVGQ 62
DB 6 SGVAVNDECMKLFGL-----QSKLHRFITFKMDKPKKEIVVDQ-----VGDRAT 51
QY 63 TVDDPYATFVKMLPKDKCRYALYDATYETKESKEDLVFIWAPESAPLKSOMIYASSK 121
DB 52 SYDD-----FTNSLPENDCRYAIYDFEYVTAEDVQKSRIFYILWSPSSAKVKSOMLYASSN 107
QY 122 DAIKKLTGKIKHELQAN-----CYBEVKDR 146
DB 108 QRFKSGINGIQVELQATDASEISLDEIKDR 137

RESULT 14

A86149

actin-depolymerizing factor homolog Atg01750 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: A86149

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;

ansen, N.P.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: A86149

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-140 <STO>

A;CROSS-references: UNIPROT:Q9LQ81; GB:AE005172; NID:g8671845; PIDN:AAF78408.1; GSPDB:GN00066

C;Genetics:

A;Map position: 1

C;Superfamily: cofillin

Query Match 25.2%; Score 213; DB 2; Length 140;
Best Local Similarity 32.5%; Pred. No. 3e-10;
Matches 50; Conservative 38; Mismatches 42; Indels 24; Gaps 5;
QY 2 ASGVAVSDGVKVFNDKMKVRKSTPEEVKKRKKAVLFCLESDKKNIIIEEGKEILVGDVG 61
DB 5 ASGMHVSDECKLKFLEK-----AKRNRVTFVKIDEKAQQWMDK-----LGNPE 50
QY 62 QTVDPPYATFVKMLPKDKCRYALYDATYETKESKEDLVFIWAPESAPLKSOMIYASS 120

```

51  ETYED-----FTRSIPEDECRVAVDYDFTTPENCQKSKIFFIAWSPTDSVRSKMLYASS 106
121  KDAIKKLTGIKHKLQANCYEE-----VKORCTL 149
107  KDRFKRLDGIQVELQATDPPEMSLDIIKGRVNL 140

```

RESULT 15

G84717
actin depolymerizing factor 6 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-feb-2001 #text_change 16-Feb-2001
C/Accession: G84717
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Eussa, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: G84717
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-132 <SFO>
A/Cross-references: GB:AE002093; NID:G432815; PIDN:AAD20665.1; GSPDB:GN00139
C/Genetics:
A/Gene: At2g31200
A/Map position: 2
C/Superfamily: cofillin

[illegible]

Search completed: May 13, 2005, 09:47:33
Job time : 39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2005, 09:29:44 ; Search time 176 Seconds
(without alignments)
482.984 Million cell updates/sec

Title: US-10-649-952A-1
Perfect score: 846
Sequence: 1 MASGAVSDGVKVFNDMKV.....CTLAELGGSAVISLEGKPL 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	841	99.4	165	1	COFI_HUMAN
2	837	98.9	165	1	COFI_RAT
3	836	98.8	165	1	COFI_PIG
4	836	98.8	165	1	COFI_SHEEP
5	834	98.6	165	1	COFI_MOUSE
6	831	98.2	229	2	Q9CX22
7	709	83.8	166	1	COFI_CHICK
8	702	83.0	166	1	COF2_MOUSE
9	699	82.6	166	1	COF2_HUMAN
10	693	81.9	166	2	Q6N2W3
11	659	77.9	168	2	Q6NX11
12	656	77.5	168	1	COF2_XENLA
13	649	76.7	168	1	COFI_XENLA
14	625.5	73.9	165	2	Q6TH32
15	615.5	72.8	164	1	DEST_CHICK
16	606.5	71.7	164	1	DEST_MOUSE
17	604.5	71.5	165	2	Q6DV06
18	601.5	71.1	164	1	DEST_HUMAN
19	601.5	71.1	164	1	DEST_PIG
20	598.5	70.7	164	2	Q7M0E3
21	392.5	46.4	163	2	Q7ZWD8
22	310.5	36.7	153	2	Q7ZXD4
23	282.5	33.4	153	2	Q6CXY0
24	280	33.1	143	2	Q9HPF7
25	276	32.6	143	2	Q6BWX4
26	273	32.3	143	2	Q6CQ22
27	271	32.0	143	2	Q759P0
28	268	31.7	143	2	Q96VU9
29	267.5	31.6	143	1	COFI_YEAST
30	265	31.3	143	2	Q6FV81
31	260	30.7	111	2	Q8N1B5

32	257.5	30.4	156	2	Q05307
33	257	30.4	137	1	ACTP_ACACA
34	254	30.0	137	1	COFI_SCHPO
35	230	27.2	137	1	COFI_DICDI
36	227.5	26.9	139	2	Q6T8D2
37	227	26.8	139	1	ADF3_MAIZE
38	224.5	26.5	146	2	Q8LCM6
39	222.5	26.3	463	2	Q6JAGO
40	220.5	26.1	139	1	ADFI_PETHY
41	220	26.0	140	2	Q9M594
42	219.5	25.9	139	1	ADFI_ARATH
43	219.5	25.9	143	1	ADP2_PETHY
44	217.5	25.7	139	1	ADP4_ARATH
45	216	25.5	139	2	Q84TB3

ALIGNMENTS

RESULT 1
COFI_HUMAN STANDARD; PRT; 165 AA.
AC P23528; Q9UCA2;
DT 01-NOV-1991 (Rel. 20, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Cofilin, non-muscle isoform (Cofilin-1) (18 kDa phosphoprotein) (p18).
GN Name=CFL1; Synonyms=CFL;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91088330; PubMed=2263493;
RA Ogawa K., Tashima M., Yumoto Y., Okuda T., Sawada H., Okuma M.,
RA Maruyama Y.;
RT "Coding sequence of human placenta cofilin cDNA.";
RL Nucleic Acids Res. 18:7169-7169(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA der Steege G., Draaijers T.G., Grootsoorten P.M., Ozinga J.,
RA Anzevino R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,
RA Buys C.H.C.M.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96393663; PubMed=8800436;
RA Gillett G.T., Fox M.F., Rowe P.S.N., Casimir C.M., Povey S.;
RT "Mapping of human non-muscle type cofilin (CFL1) to chromosome 11q13
and muscle-type cofilin (CFL2) to chromosome 14.";
RL Ann. Hum. Genet. 60:201-211(1996).
RN [4]
RP SEQUENCE FROM N.A.
RT TISSUE=Lung, Ovary, Placenta, and Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,

Q05307	saccharomyc
P37167	acanthamoeb
P78929	schizosacch
P54706	dictyosteli
Q6T8D2	heliathanus
Q41764	zea mays (m
Q8LCM6	arabidopsis
Q6JAGO	sorghum bic
Q9FV12	petunia hyb
Q9M594	elaeis guin
Q39250	arabidopsis
Q9FV11	petunia hyb
Q9ZK3	arabidopsis
Q84TB3	oryza sativ

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP (5)
RQ SEQUENCE OF 1-20.
RT TISSUE=Platelet;
RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
RQ Thomas G.R., Vandekerckhove J.;
RT "Exploring proteomes and analyzing protein processing by mass
RL spectrometric identification of sorted N-terminal peptides";
RN Nat. Biotechnol. 21:566-569 (2003).
RP (6)
RQ SEQUENCE OF 51-70.
RT TISSUE=Platelet;
RX MEDLINE=94311852; PubMed=8037689;
RA Davidson M.M., Haslam R.J.;
RT "Dephosphorylation of cofilin in stimulated platelets: roles for a
RL GTP-binding protein and Ca2+";
RN Biochem. J. 301:41-47 (1994).
RP (1)
RQ -1- FUNCTION: Controls reversibly actin polymerization and
RT depolymerization in a pH-sensitive manner. It has the ability to
RX bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
RA major component of intranuclear and cytoplasmic actin rods.
RQ -1- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic; almost
RT completely in nucleus in cells exposed to heat shock or 10%
RL dimethyl sulfoxide.
RN -1- TISSUE SPECIFICITY: Widely distributed in various tissues.
RP -1- PTM: The phosphorylation of Ser-23 may prevent recognition of the
RQ nuclear localization signal.
RX -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
RA This SWISS-PROT entry is copyright. It is produced through a collaboration
RQ between the Swiss Institute of Bioinformatics and the EMBL outstation -
RX the European Bioinformatics Institute. There are no restrictions on its
RA use by non-profit institutions as long as its content is in no way
RQ modified and this statement is not removed. Usage by and for commercial
RT entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
RL or send an email to license@isb-sib.ch).
RP (1)
RQ EMBL; D00682; BAA00589.1; -
RX EMBL; U21909; AAA64501.1; -
RA EMBL; X95404; CAA64685.1; -
RQ EMBL; BC011005; AAH11005.1; -
RX EMBL; BC012285; AAH12285.1; -
RA EMBL; BC012318; AAH12318.1; -
RQ EMBL; BC018256; AAH18256.1; -
RX PIR; S12632; S12632.
RA HSSP; P18282; IAK6.
RQ SWISS-2DPAGE; P23528; HUMAN.
RX Aarhus/Ghent-2DPAGE; 4; IEF.
RA OGP; P23528; -
RQ Genew; HGNC:1874; CFL1.
RX H-InvDB; HIX0009808; -
RA MIM; 601442; -
RQ GO; GO:0005634; C:nucleus; TAS.
RX GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; TAS.
RA GO; GO:0007266; P:rho protein signal transduction; TAS.
RQ InterPro; IPR002108; Actbind_cofin.
RX Pfam; PF00241; Cofilin_ADF; 1.
RA PRINTS; PR00006; COFILIN.
RQ ProDom; PD002129; Actbind_cofin; 1.
RX SMART; SW00102; ADF; 1.
RA PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
RQ Actin-binding; Cytoskeleton; Direct protein sequencing;
RX Nuclear protein; Phosphorylation.
RA INIT MET 0
RQ DONA1N 29 33 Nuclear localization signal (Potential).
RX DONA1N 105 124 Actin-binding (Potential).
RA MOD RES 23 23 Phosphoserine (Probable).
RQ SEQUENCE 165 AA; 18371 MW; EC9251A6D1C7C84C CRC64;
SQ

Query Match 99.4%; Score 841; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 6.9e-62;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ASGVAVSDGVKVFNDMKVKSSTPEHVKKRKAIVLFCISDKKNIILBEGKEILVDVG 61
DB 1 ASGVAVSDGVKVFNDMKVKSSTPEHVKKRKAIVLFCISDKKNIILBEGKEILVDVG 60
QY 62 QTVDVDPVATFVKMLPKDKCRVYALDYATYETKESKEDLVFIWFAPESAPLKSMMIYASSK 121
DB 61 QTVDVDPVATFVKMLPKDKCRVYALDYATYETKESKEDLVFIWFAPESAPLKSMMIYASSK 120
QY 122 DAIKKKLITGKHELOANCYEEVKDRCTLAELGGSAVISLEGKPL 166
DB 121 DAIKKKLITGKHELOANCYEEVKDRCTLAELGGSAVISLEGKPL 165
RESULT 2
COFI_RAT
ID_COF1_RAT STANDARD; PRT; 165 AA.
AC P45592;
DT 01-NOV-1995 (Rel. 32, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cofilin, non-muscle isoform (Cofilin-1).
GN Names=Cfil1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RA Shirasawa T., Takahashi H., Sakamoto K., Kawashima A., Akashi T.;
RL Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE, ACETYLATION, PHOSPHORYLATION SITE SER-23, AND MASS
RQ SPECTROMETRY.
RC TISSUE=Parotid gland;
RA Kanamori T., Suzuki M.M., Titani K.;
RT "Complete amino acid sequences and phosphorylation sites, determined
RL by Edman degradation and mass spectrometry, of rat parotid destrin-and
RQ cofilin-like protein";
RX Submitted (AUG-1998) to the PIR data bank.
CC -1- FUNCTION: Controls reversibly actin polymerization and
CC depolymerization in a pH-sensitive manner. It has the ability to
CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
CC major component of intranuclear and cytoplasmic actin rods (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By
CC similarity).
CC -1- TISSUE SPECIFICITY: Widely distributed in various tissues (By
CC similarity).
CC -1- PTM: The phosphorylation of Ser-23 may prevent recognition of the
CC nuclear localization signal.
CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
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CC or send an email to license@isb-sib.ch).
CC (1)
CC EMBL; X62908; CAA44694.1; -
CC PIR; S49101; S49101.
CC HSSP; P18282; IAK6.
CC RGD; 69285; Cfil1.
CC InterPro; IPR002108; Actbind_cofin.
CC Pfam; PF00241; Cofilin_ADF; 1.
CC PRINTS; PR00006; COFILIN.
CC ProDom; PD002129; Actbind_cofin; 1.

DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
 KW Acetylation; Actin-binding; Cytoskeleton; Direct protein sequencing;
 KW Nuclear protein; Phosphorylation.
 FT INIT MET 0 0
 FT MOD_RES 1 1 N-acetyllalanine.
 FT DOMAIN 29 33 Nuclear localization signal (Potential).
 FT DOMAIN 105 124 Actin-binding (Potential).
 FT MOD_RES 23 23 Phosphoserine.
 SQ SEQUENCE 165 AA; AD8FFACB671CA5E7 CRC64;
 Query Match 98.9%; Score 837; DB 1; Length 165;
 Best Local Similarity 99.4%; Pred. No. 1.5e-61;
 Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ASGVAVSDGVKVFNDMKVRKSTPEEVKRRKKAFLCLSEDKKNILLEGKEILVGDVG 61
 DB 1 ASGVAVSDGVKVFNDMKVRKSTPEEVKRRKKAFLCLSEDKKNILLEGKEILVGDVG 60
 QY 62 QTVDPPYATFVKMLPDCKRYALYDATTETKSKEDLVFIWAPESAPLKSMMIYASSK 121
 DB 61 QTVDPPYATFVKMLPDCKRYALYDATTETKSKEDLVFIWAPESAPLKSMMIYASSK 120
 QY 122 DAIKKKLTGKHLEQANCYEEVKDRTLAELGSSAVISLEGKPL 166
 DB 121 DAIKKKLTGKHLEQANCYEEVKDRTLAELGSSAVISLEGKPL 165
 RESULT 3
 COPI_PIG
 ID COPI_PIG STANDARD; PRT; 165 AA.
 AC P10668; Q29374;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 25-JAN-2005 (Rel. 46, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Cofilin, non-muscle isoform (Cofilin-1).
 GN Name=CFL1;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=88298817; PubMed=3403546;
 RA Matsuzaki F., Matsumoto S., Yahara I., Yonezawa N., Nishida E.,
 Sakai H.;
 RT "Cloning and characterization of porcine brain cofilin cDNA. Cofilin
 contains the nuclear transport signal sequence.";
 RL J. Biol. Chem. 263:11564-11568(1988).
 RN [2]
 RP SEQUENCE OF 1-103 FROM N.A.
 RC TISSUE=Small intestine;
 RX MEDLINE=96327607; PubMed=8672129;
 RA Winteroe A.K., Fredholm M., Davies W.;
 RT "Evaluation and characterization of a porcine small intestine CDNA
 library: analysis of 839 clones.";
 RL Mamm. Genome 7:509-517(1996).
 CC -!- FUNCTION: Controls reversibly actin polymerization and
 depolymerization in a pH-sensitive manner. It has the ability to
 bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
 major component of intranuclear and cytoplasmic actin rods.
 CC -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic; almost
 completely in nucleus in cells exposed to heat shock or 10%
 dimethyl sulfoxide.
 CC -!- TISSUE SPECIFICITY: Widely distributed in various tissues.
 CC -!- PTM: The phosphorylation of Ser-23 may prevent recognition of the
 nuclear localization signal.
 CC -!- MISCELLANEOUS: A double mutation of Lys-111 and Lys-113 to Gln
 produces a mutant with no ability to depolymerize or bind F-actin.
 CC -!- SIMILARITY: Belongs to the actin-binding proteins ADF family.
 CC -----
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 CC -----
 DR EMBL; M20866; AAA31020.1; -;
 DR EMBL; F14577; CAA23134.1; -;
 DR PIR; A29240; A29240.
 DR HSSP; P18282; 1AK6.
 DR InterPro; IPR002108; Actbind cofiln.
 DR Pfam; PF00241; Cofilin_ADF; 1.
 DR PRINTS; PR00006; COFILIN.
 DR ProDom; PD002129; Actbind_cofiln; 1.
 DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
 KW Actin-binding; Cytoskeleton; Direct protein sequencing;
 KW Nuclear protein; Phosphorylation.
 FT INIT MET 0 0 By similarity.
 FT DOMAIN 29 33 Nuclear localization signal (Potential).
 FT DOMAIN 105 124 Actin-binding (Potential).
 FT MOD_RES 23 23 Phosphoserine (By similarity).
 FT MUTAGEN 111 111 K->Q: Slight modification of activity.
 FT MUTAGEN 113 113 K->Q: Impairs interaction with actin.
 SQ SEQUENCE 165 AA; 18387 MW; EC9241B6D1D7D84C CRC64;
 Query Match 98.8%; Score 836; DB 1; Length 165;
 Best Local Similarity 99.4%; Pred. No. 1.8e-61;
 Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ASGVAVSDGVKVFNDMKVRKSTPEEVKRRKKAFLCLSEDKKNILLEGKEILVGDVG 61
 DB 1 ASGVAVSDGVKVFNDMKVRKSTPEEVKRRKKAFLCLSEDKKNILLEGKEILVGDVG 60
 QY 62 QTVDPPYATFVKMLPDCKRYALYDATTETKSKEDLVFIWAPESAPLKSMMIYASSK 121
 DB 61 QTVDPPYATFVKMLPDCKRYALYDATTETKSKEDLVFIWAPESAPLKSMMIYASSK 120
 QY 122 DAIKKKLTGKHLEQANCYEEVKDRTLAELGSSAVISLEGKPL 166
 DB 121 DAIKKKLTGKHLEQANCYEEVKDRTLAELGSSAVISLEGKPL 165
 RESULT 4
 COPI_SHEEP
 ID COPI_SHEEP STANDARD; PRT; 165 AA.
 AC Q6B7M7;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-JAN-2005 (Rel. 46, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Cofilin, non-muscle isoform (Cofilin-1).
 GN Name=CFL1;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Endometrium;
 RA Welker J.E., Ott T.L.;
 RT "Cloning and characterization of cofilin-1 expression in cyclic and
 early pregnant ovine endometrium following isolation by yeast-two
 hybrid screening.";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Controls reversibly actin polymerization and
 depolymerization in a pH-sensitive manner. It has the ability to
 bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
 major component of intranuclear and cytoplasmic actin rods (By
 similarity).
 CC -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By
 similarity).

CC -!- PTM: The phosphorylation of Ser-23 may prevent recognition of the
 CC nuclear localization signal (By similarity).
 CC -!- SIMILARITY: Belongs to the actin-binding proteins ADP family.
 CC
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 CC
 CC EMBL; AY676116; AAT77679.1; -
 CC PRODom; PD002129; Actbind coflin; 1.
 CC PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
 CC Actin-binding; Cytoskeleton; Nuclear protein; Phosphorylation.
 CC INIT MET 0 By similarity.
 CC DOMAIN 29 33 Nuclear localization signal (Potential).
 CC FT 105 124 Actin-binding (Potential).
 CC FT MOD RES 23 23 Phosphoserine (By similarity).
 CC SQ SEQUENCE 165 AA; 18387 MW; EC9241B6D1D7D84C CRC64;

Query Match 98.8%; Score 836; DB 1; Length 165;
 Best Local Similarity 99.4%; Pred. No. 1.8e-61;
 Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASGVAVSDGVTKVFNMDKVRKSSPTPEVKRKKAVLFCLSEDKNIIILRGKELVGDVG 61

Db 1 ASGVAVSDGVTKVFNMDKVRKSSPTPEVKRKKAVLFCLSEDKNIIILRGKELVGDVG 60

QY 62 QTVDPPYATFVKMLPDKCRVALYDATTYETKSKEDLVFIWAPESAPLKSMMIYASSK 121

Db 61 QTVDPPYATFVKMLPDKCRVALYDATTYETKSKEDLVFIWAPESAPLKSMMIYASSK 120

QY 122 DAIKKKLTGKHELOQANCYEEVKDRCTLAELKLGSAVISLEGKPL 166

Db 121 DAIKKKLTGKHELOQANCYEEVKDRCTLAELKLGSAVISLEGKPL 165

RESULT 5

ID COFI_MOUSE STANDARD; PRT; 165 AA.
 AC P18760;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 25-JAN-2005 (Rel. 46, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Cofilin, non-muscle isoform (Cofilin-1).
 GN Name=Cfli;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.
 STRAIN=C57BL/6; TISSUE=Brain;
 MEDLINE=22388257; PubMed=2349104;
 MEDLINE=90272419; PubMed=2349104;
 RA Moriyama K., Matsunoto S., Nishida E., Sakai H., Yahara I.;
 RL "Nucleotide sequence of mouse cofilin cDNA";
 RL Nucleic Acids Res. 18:3053-3053(1990).
 [2]

SEQUENCE FROM N.A.

STRAIN=C57BL/6; TISSUE=Brain;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Controls reversibly actin polymerization and
 CC depolymerization in a pH-sensitive manner. It has the ability to
 CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
 CC major component of intranuclear and cytoplasmic actin rods.
 CC -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic; almost
 CC completely in nucleus in cells exposed to heat shock or 10%
 CC dimethyl sulfoxide.
 CC -!- TISSUE SPECIFICITY: Widely distributed in various tissues.
 CC -!- PTM: The phosphorylation of Ser-23 may prevent recognition of the
 CC nuclear localization signal.
 CC -!- SIMILARITY: Belongs to the actin-binding proteins ADP family.
 CC
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 CC
 CC EMBL; D00472; BAA00364.1; -
 CC EMBL; BC058726; AAH58726.1; -
 CC PIR; S12584; S12584.
 CC HSP; P18282; IAK6.
 CC SWISS-2DPAGE; P18760; MOUSE.
 CC MGD; MGI:101757; Cfli.
 CC InterPro; IPR002108; Actbind coflin.
 CC Pfam; PF00241; Cofilin ADF; 1.
 CC PRINTS; PR00006; COFILIN.
 CC PRODom; PD002129; Actbind coflin; 1.
 CC PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
 CC Actin-binding; Cytoskeleton; Nuclear protein; Phosphorylation.
 CC INIT MET 0 By similarity.
 CC DOMAIN 29 33 Nuclear localization signal (Potential).
 CC FT 105 124 Actin-binding (Potential).
 CC FT MOD RES 23 23 Phosphoserine (By similarity).
 CC SQ SEQUENCE 165 AA; 18428 MW; AD8FE7D66701B8E7 CRC64;

Query Match 98.6%; Score 834; DB 1; Length 165;
 Best Local Similarity 98.8%; Pred. No. 2.6e-61;
 Matches 163; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASGVAVSDGVTKVFNMDKVRKSSPTPEVKRKKAVLFCLSEDKNIIILRGKELVGDVG 61

Db 1 ASGVAVSDGVTKVFNMDKVRKSSPTPEVKRKKAVLFCLSEDKNIIILRGKELVGDVG 60

QY 62 QTVDPPYATFVKMLPDKCRVALYDATTYETKSKEDLVFIWAPESAPLKSMMIYASSK 121

Db 61 QTVDPPYATFVKMLPDKCRVALYDATTYETKSKEDLVFIWAPESAPLKSMMIYASSK 120

QY 122 DAIKKKLTGKHELOQANCYEEVKDRCTLAELKLGSAVISLEGKPL 166

Db 121 DAIKKKLTGKHELOQANCYEEVKDRCTLAELKLGSAVISLEGKPL 165

RESULT 6

ID Q9CX22 PRELIMINARY; PRT; 229 AA.
 AC Q9CX22; 2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 12 days embryo embryonic body between diaphragm region

DE and neck cDNA, RIKEN full-length enriched library, clone:9430060001
DE product:cofilin 1, non-muscle, full insert sequence.
GN Names=Cfil1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RC MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RA "high-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RC MEDLINE=2050913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK020471; BAB32114.1; -.
DR HSSP; P60982; 1AK6.
DR MGI; 101757; Cfil1.
DR GO; GO:0030864; C:cortical actin cytoskeleton; IDA.
DR InterPro; IPR002108; Actbind_cofln.
DR Pfam; PF00241; Cofilin_ADF; I.
DR PRINTS; PR00006; COFILIN.
DR PRODOM; PD002129; Actbind_cofln; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
SQ SEQUENCE 229 AA; 24795 MW; 1198E9A8F166B75 CRC64;

Query Match 98.2%; Score 831; DB 2; Length 229;
Best Local Similarity 98.2%; Pred. No. 6.8e-61;
Matches 162; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MASGVAVSQGVKIVFNDKVRKSTPEEVKRRKAVLFCLSSEDKKNILLEGKEILVGDV 60
DB 1 MASGVAVSQGVKIVFNDKVRKSTPEEVKRRKAVLFCLSSEDKKNILLEGKEILVGDV 60

QY 61 GQTVDDPYATFVKMLPDKCRVALYDATYETKSKKEDLVFIWAPESAPLKSVMYASS 120
DB 61 GQTVDDPYATFVKMLPDKCRVALYDATYETKSKKEDLVFIWAPENAPLKSVMYASS 120

QY 121 KDAKKKLTGKIKHELOANCYEEVKDRTLAELGGSVAVISLEGP 165
DB 121 KDAKKKLTGKIKHELOANCYEEVKDRTLAELGGSVAVISLEGP 165

RESULT 7
COFI_CHICK STANDARD; PRT; 166 AA.
ID COFI_CHICK
AC P21566;
DT 01-MAY-1991 (Rel. 18, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cofilin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RC MEDLINE=91027755; PubMed=1699599;
RA Abe H., Endo T., Yamamoto K., Obinata T.;
RT "Sequence of cDNAs encoding actin depolymerizing factor and cofilin of
RT embryonic chicken skeletal muscle: two functionally distinct actin-
RT regulatory proteins exhibit high structural homology.";
RL Biochemistry 29:7420-7425(1990).
RN [2]
RP STRUCTURE BY NMR, AND REVISIONS TO 53-54.
RX MEDLINE=21880669; PubMed=11885570; DOI=10.1023/A:1014227808686;
RA Bains N.P.S., Gorbatyuk V.Y., Nosworthy N.J., Robson S.A.,
RA Mactejewski M.W., dos Remedios C.G., King G.F.;
RT "Backbone and side-chain 1H, 15N, and 13C assignments for chick
RT cofilin.";
RL J. Biomol. NMR 22:193-194(2002).
CC -!- FUNCTION: Controls reversibly actin polymerization and
CC depolymerization in a pH-sensitive manner. It has the ability to
CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
CC major component of intranuclear and cytoplasmic actin rods.
CC -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic; almost
CC completely in nucleus in cells exposed to heat shock or 10%
CC dimethyl sulfoxide.
CC -!- TISSUE SPECIFICITY: Widely distributed in various tissues.
CC -!- PTM: The phosphorylation of Ser-24 may prevent recognition of the
CC nuclear localization signal.
CC -!- SIMILARITY: Belongs to the actin-binding proteins ADF family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

[1]
 SEQUENCE FROM N.A.
 Jin J., Li G., Hu S., Li W., Yuan J., Qiang B.,
 "Isolation of two isoforms of human cofilin cDNA."
 Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 SEQUENCE FROM N.A.
 MEDLINE=21315834; PubMed=11422377;
 Thirion C., Stucka R., Mendel B., Gruhler A., Jaksch M., Nowak K.J.,
 Binz N., Laing N.G., Lochmuller H.,
 "Characterization of human muscle type cofilin (CFL2) in normal and
 regenerating muscle."
 Eur. J. Biochem. 268:3473-3482(2001).
 [3]
 SEQUENCE FROM N.A.
 TISSUE=Bone marrow, Placenta, and Skeletal muscle;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 -!- FUNCTION: Controls reversibly actin polymerization and
 depolymerization in a pH-sensitive manner. It has the ability to
 bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
 major component of intranuclear and cytoplasmic actin rods (By
 similarity).
 -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By
 similarity).
 -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Comment=isoforms are identical at the level of the protein
 sequence;
 Name=CFL2b;
 IsoId=Q9Y281-1; Sequence=Displayed;
 Name=CFL2a;
 IsoId=Q9Y281-2; Sequence=Not described;
 -!- TISSUE SPECIFICITY: Isoform CFL2b is expressed predominantly in
 skeletal muscle and heart, while isoform CFL2a is expressed in
 various tissues.
 -!- PTM: The phosphorylation of Ser-24 may prevent recognition of the
 nuclear localization signal.
 -!- SIMILARITY: Belongs to the actin-binding proteins ADF family.

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 or send an email to license@isb-sib.ch).

 EMBL; AF134802; AAD31280.1; -
 EMBL; AF134803; AAD31281.1; -
 EMBL; AF283513; AAF97934.1; -
 EMBL; AF242229; AAF64498.1; -
 EMBL; BC011444; AAH1444.1; -
 EMBL; BC022364; AAH22364.1; -

DR EMBL; BC022876; AAH22876.1; -
 DR HSSP; PI8282; 1AKG.
 DR Genew; HGNC:1875; CFL2.
 DR MIM; 601443; -
 DR InterPro: IPR002108; Actbind cofln.
 DR Pfam; PF00241; Cofilin_ADF; 1.
 DR PRINTS; PRO0006; COFILIN.
 DR ProDom; PD002129; Actbind_cofln; 1.
 DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
 KW Actin-binding; Alternative splicing; Cytoskeleton; Nuclear protein;
 KW Phosphorylation.
 FT DOMAIN 30 34 Nuclear localization signal (Potential).
 FT DOMAIN 106 125 Actin-binding (Potential).
 FT MOD RES 24 24 Phosphoserine (By similarity).
 SQ SEQUENCE 166 AA; 18736 MW; 48B6DCCAB9FE1CC CRC64;
 Query Match 82.6%; Score 699; DB 1; Length 166;
 Best Local Similarity 80.7%; Pred. No. 4e-50;
 Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MASGVAVSDGVKVFNDMKVRKSSSTPEEVKKKAVLFCLSDDKKNIIIEEGKEILVGDV 60
 DB 1 MASGVTVNDGVKVFNDMKVRKSSSTQEEIKKKKAVLFCLSDDKQRIIVVEAKQILVGD 60
 QY 61 GOTVDDPYATFVKMLPDKCRVALYDQYATYETKESKEDLVFIWAPESAPLSKMIYASS 120
 DB 61 GDTVEDPYTSFKLLPLNDCRYALYDQYATYETKESKEDLVFIWAPESAPLSKMIYASS 120
 QY 121 KDAIKKLTGIGHELOANCYEEVKRCITLAEKLGSAVISLEGKPL 166
 DB 121 KDAIKKKTGIGKHEQVNGVLDIDKDRSTLGEKLGNNVVVSLGKPL 166
 RESULT 10
 Q6NZW3 PRELIMINARY; PRT; 166 AA.
 AC Q6NZW3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Cofilin 2 (Muscle).
 GN Name=cfl2;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E.,
 Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 -!- FUNCTION: Controls reversibly actin polymerization and
 depolymerization in a pH-sensitive manner. It has the ability to
 bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
 major component of intranuclear and cytoplasmic actin rods (By
 similarity).
 -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By
 similarity).
 -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Comment=isoforms are identical at the level of the protein
 sequence;
 Name=CFL2b;
 IsoId=Q9Y281-1; Sequence=Displayed;
 Name=CFL2a;
 IsoId=Q9Y281-2; Sequence=Not described;
 -!- TISSUE SPECIFICITY: Isoform CFL2b is expressed predominantly in
 skeletal muscle and heart, while isoform CFL2a is expressed in
 various tissues.
 -!- PTM: The phosphorylation of Ser-24 may prevent recognition of the
 nuclear localization signal.
 -!- SIMILARITY: Belongs to the actin-binding proteins ADF family.

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 or send an email to license@isb-sib.ch).

 EMBL; AF134802; AAD31280.1; -
 EMBL; AF134803; AAD31281.1; -
 EMBL; AF283513; AAF97934.1; -
 EMBL; AF242229; AAF64498.1; -
 EMBL; BC011444; AAH1444.1; -
 EMBL; BC022364; AAH22364.1; -

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RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065947; AAH65947.1; -.
DR HSP; P60982; IAK6.
DR ZFIN; ZDB-GENE-040426-1815; cfl2.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; Cofilin_ADF; I.
DR PRINTS; PR00006; COFILIN.
DR PRODOM; PD002129; Actbind_cofin; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
SQ SEQUENCE 166 AA; 18568 MW; 795942E0F8FOA2D6 CRC64;

Query Match 81.9%; Score 693; DB 2; Length 166;
Best Local Similarity 80.1%; Pred. No. 1.3e-49;
Matches 133; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVKVFNDKVRKSTPEEVKRRKAVLFCLSDDKKNILLEGKEILVGDV 60
Db 1 MASGTVSDGVKVFNDKVRKSSDEVKRRKAVLFCLSDDKKNILLEGKEILVGDV 60

Qy 61 GQTVDDPYATFVKMLPKDCRYALYDATTYETKESKEDLVFIWAPESAPLKSMMIYASS 120
Db 61 GDSVDDPYATFVKMLPKDCRYALYDATTYETKESKEDLVFIWAPESAPLKSMMIYASS 120

Qy 121 KDAIKKLTGKIHQLQANCYEEVDRCTLAELGGSVAIVSLEKPL 166
Db 121 KDAIKKLTGKIHQLQANCYEEVDRCTLAELGGSVAIVSLEKPL 166

RESULT 11
Q6NX11 PRELIMINARY; PRT; 168 AA.
AC Q6NX11;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC76274.
GN Name=MGC76274;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smallus D.E., Schnertch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RN [2] and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067328; AAH67328.1; -.
DR HSP; P60982; IAK6.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; Cofilin_ADF; I.
DR PRINTS; PR00006; COFILIN.
DR PRODOM; PD002129; Actbind_cofin; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
SQ SEQUENCE 168 AA; 19073 MW; 14AB09FF9616496A CRC64;

Query Match 77.9%; Score 659; DB 2; Length 168;
Best Local Similarity 78.3%; Pred. No. 8.4e-47;
Matches 130; Conservative 8; Mismatches 28; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVKVFNDKVRKSTPEEVKRRKAVLFCLSDDKKNILLEGKEILVGDV 60
Db 1 MASGVMVSDGVKVFNDKVRHQLSPPEAKRRKAVVFCLSDDKKNILLEGKEILVGDV 60

Qy 61 GQTVDDPYATFVKMLPKDCRYALYDATTYETKESKEDLVFIWAPESAPLKSMMIYASS 120
Db 61 GCVNDDPYATFVKMLPKDCRYALYDATTYETKESKEDLVFIWAPESAPLKSMMIYASS 120

Qy 121 KDAIKKLTGKIHQLQANCYEEVDRCTLAELGGSVAIVSLEKPL 166
Db 121 KDAIKKLTGKIHQLQANCYEEVDRCTLAELGGSVAIVSLEKPL 166

RESULT 12
Q6F2_XENLA STANDARD; PRT; 168 AA.
AC P45593;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cofilin 2.
GN Name=XAC2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96180281; PubMed=8603919; DOI=10.1083/jcb.132.5.871;
RA Abe H., Obinata T., Minamide L.S., Bamberg J.R.;
RT "Xenopus laevis actin-depolymerizing factor/cofilin: a
RT phosphorylation-regulated protein essential for development.";
RN J. Cell Biol. 132:871-885(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RA Wada A., Gotoh Y., Nishida E.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Controls reversibly actin polymerization and
CC depolymerization in a pH-sensitive manner. It has the ability to
CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
CC major component of intranuclear and cytoplasmic actin rods (By
CC similarity).
CC -I- SUBCELLULAR LOCATION: Intracellular and cytoplasmic (By
CC similarity).
CC -I- SIMILARITY: Belongs to the actin-binding proteins ADF family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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EMBL: U26269; AAB00539.1; -.
 EMBL: D38406; BAA07461.1; -.
 HSSP: P18282; 1AK6.
 InterPro: IPR002108; Actbind_cofln.
 Pfam: PF00241; Cofilin_ADF; 1.
 PRINTS: PR00006; COFILIN.
 ProDom: PD002129; Actbind_cofln; 1.
 SMART: SM00102; ADF; 1.
 PROSITE: PS00325; ACTIN_DEPOLYMERIZING; 1.
 Actin-binding; Cytoskeleton; Nuclear localization signal (Potential).
 FT DOMAIN 30 34
 DOMAIN 106 125 Actin-binding (Potential).
 SQ SEQUENCE 168 AA; 19120 MW; 6DBC7F8397EDFD1 CRC64;

Query Match 77.5%; Score 656; DB 1; Length 168;
 Best Local Similarity 75.3%; Pred. No. 1.5e-46;
 Matches 125; Conservative 15; Mismatches 26; Indels 0; Gaps 0;

QY 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKKAVLFCLSDDKKNIIIEEGKEILVGDV 60
 DB 1 MASGVWSDVVKVFNDKVRKSTPEEVKKKAVLFCLSDDKKNIIIEEGKEILVGDV 60

QY 61 GQTVDDPYATFVKMLPDKDCRYALYDITYETKESKKEDLVFIFWAPESAPLKSMMIYASS 120
 DB 61 GCNVEDPYKTFVKMLPRNDCRYALYDITYETKESKKEDLVFIFWAPESAPLKSMMIYASS 120

QY 121 KDAIKKLTGKHELOQANCYEEVKDRCCTLAELKGGSAVISLEGK 166
 DB 121 KDAIKRFTGKHEWQNTYDDINDPCNLADKLGNTVVSLEGKSL 166

RESULT 13
 COPI_XENLA STANDARD; PRT; 168 AA.
 AC P45695;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cofilin 1.
 GN Name=XAC1;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=96180281; PubMed=8603919; DOI=10.1083/jcb.132.5.871;
 RA Abe H., Obinata T., Minamide L.S., Bamberg J.R.
 RT "Xenopus laevis actin-depolymerizing factor/cofilin: a phosphorylation-regulated protein essential for development.";
 RL J. Cell Biol. 132:871-885(1996).
 CC -!- FUNCTION: Controls reversibly actin polymerization and depolymerization in a pH-sensitive manner. It has the ability to bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the major component of intranuclear and cytoplasmic actin rods (by similarity).
 CC -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the actin-binding proteins ADF family.

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EMBL: U26270; AAB00540.1; -.
 HSSP: P18282; 1AK6.
 InterPro: IPR002108; Actbind_cofln.
 Pfam: PF00241; Cofilin_ADF; 1.
 PRINTS: PR00006; COFILIN.
 ProDom: PD002129; Actbind_cofln; 1.
 SMART: SM00102; ADF; 1.
 PROSITE: PS00325; ACTIN_DEPOLYMERIZING; 1.
 Actin-binding; Cytoskeleton; Nuclear localization signal (Potential).
 FT DOMAIN 30 34
 DOMAIN 106 125 Actin-binding (Potential).
 SQ SEQUENCE 168 AA; 19066 MW; F3A4D8635A3683D6 CRC64;

Query Match 76.7%; Score 649; DB 1; Length 168;
 Best Local Similarity 76.2%; Pred. No. 5.7e-46;
 Matches 125; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

QY 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKKAVLFCLSDDKKNIIIEEGKEILVGDV 60
 DB 1 MASGVWSDVVKVFNDKVRKSTPEEVKKKAVLFCLSDDKKNIIIEEGKEILVGDV 60

QY 61 GQTVDDPYATFVKMLPDKDCRYALYDITYETKESKKEDLVFIFWAPESAPLKSMMIYASS 120
 DB 61 GCNVEDPYKTFVKMLPRNDCRYALYDITYETKESKKEDLVFIFWAPESAPLKSMMIYASS 120

QY 121 KDAIKKLTGKHELOQANCYEEVKDRCCTLAELKGGSAVISLEGK 164
 DB 121 KDAIKRLLPGIKHEWQINTYEDVNDPCNLADKLGNTVVSLEGK 164

RESULT 14
 Q6TH32 PRELIMINARY; PRT; 165 AA.
 AC Q6TH32;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Muscle cofilin 2.
 GN Name=cfil2l; Synonym=CFL2;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 SEQUENCE FROM N.A.
 RC TISSUE=Kidney marrow;
 RA Song H.D., Wu X.Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
 RA Sheng Y., Chen Y., Ruan Z., Jiang C.L., Fan H.Y., Zou L.I.,
 RA Kanki J.P., Look A.T., Chen Z.
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBSJ databases.
 DR EMBL: AY398324; AAO97757.1; -.
 DR HSSP: P60982; 1AK6.
 DR ZFIN: ZDB-GENE-030131-215; cfil2l.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0003779; F:actin binding; IEA.
 DR InterPro: IPR002108; Actbind_cofln.
 DR Pfam: PF00241; Cofilin_ADF; 1.
 DR PRINTS: PR00006; COFILIN.
 DR ProDom: PD002129; Actbind_cofln; 1.
 DR SMART: SM00102; ADF; 1.
 DR PROSITE: PS00325; ACTIN_DEPOLYMERIZING; 1.
 SQ SEQUENCE 165 AA; 18771 MW; 3PD3F8F542E2A707 CRC64;

Query Match 73.9%; Score 625.5; DB 2; Length 165;
 Best Local Similarity 74.9%; Pred. No. 4.9e-44;
 Matches 125; Conservative 17; Mismatches 20; Indels 5; Gaps 2;

QY 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKKAVLFCLSDDKKNIIIEEGKEILVGDV 59
 DB 1 MASGVTVETVLTVFNDKVRKSTPEEVKKKAVLFCLSDDKKNIIIEEGKEILVGDV 60

QY 60 VQQTVDPPYATFVKMLPDKDCRYALYDITYETKESKKEDLVFIFWAPESAPLKSMMIYASS 119

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Db 61 EG-----DPLKFKVQLPNDCRYALYDATYETKTKEDLVFIWAPESAPLKSMMIYAS 116
QY 120 SKDAIKKKLTGKIKHELQANCVEEVKDRCTLAELGGSAVISLEGKPL 166
Db 117 SKDAIKKKKFTGKIKHEWQVNGMDIKDRKTLAELGGASVVSLEGKPL 163

RESULT 15
ID DEST CHICK STANDARD; PRT; 164 AA.
AC P18359;
DT 01-NOV-1990 (Rel. 16, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DE Destrin (Actin-depolymerizing factor) (ADF).
GN Name=DSTN; Synonyms=DSN;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 100-110 AND 115-133.
RP TISSUE=Brain;
RX MEDLINE=91027754; PubMed=2223773;
RA Adams M.E., Minamide L.S., Duester G., Bamberg J.R.;
RT "Nucleotide sequence and expression of a cDNA encoding chick brain
actin depolymerizing factor.";
RL Biochemistry 29:7414-7420(1990).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Skeletal muscle;
RX MEDLINE=91027755; PubMed=1699599;
RA Abe H., Endo T., Yamamoto K., Obinata T.;
RT "Sequence of cDNAs encoding actin depolymerizing factor and cofilin of
embryonic chicken skeletal muscle: two functionally distinct actin-
regulatory proteins exhibit high structural homology.";
RL Biochemistry 29:7420-7425(1990).
CC -1- FUNCTION: Actin-depolymerizing protein. Severs actin filaments (F-
actin) and binds to actin monomers (G-actin). Acts in a pH-
independent manner.
CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J02912; AAA48575.1; -.
DR EMBL; M55660; AAA48573.1; -.
DR PIR; A35702; A35702.
DR HSSP; P18282; 1AK6.
DR InterPro; IPR002108; Actbind_cofln.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Actbind_cofln; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
KW Actin-binding; Direct protein sequencing.
FT INIT_MET 0 By similarity.
FT DOMAIN 29 33 Nuclear localization signal (Potential).
FT DOMAIN 105 124 Actin-binding (Potential).
SQ SEQUENCE 164 AA; 18401 MW; 72747A1D43E6E3E9 CRC64;
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Query Match 72.8%; Score 615.5; DB 1; Length 164;
Best Local Similarity 73.3%; Fred. No. 3.3e-43;
Matches 121; Conservative 18; Mismatches 25; Indels 1; Gaps 1;
OY 2 ASGVAVSDGVKVFNDKVRKSTPEVKRKKAVLFCLSBDKKNIILEGKELVGDVG 61
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Db 1 ASGVQVADVEVCRIFYDMKVRKCTPEEVKRRKXAVIFCLSPDKKCIIVEGKEILVGDVG 60
QY 62 QTVDPPYATFVKMLPDKDCRYALYDASYETKESKEDLVFIWAPESAPLKSMMIYASSK 121
Db 61 VTTVDPPFKHFVEMLPKDCRYALYDASFETKESKGBELMFLWAPEQAPLKSMMIYASSK 120
QY 122 DAIKKKLTGKIKHELQANCVEEVKDRCTLAELGGSAVISLEGKPL 166
Db 121 DAIKKKFQGIKHECQANGPEDLNRAK-IAEKJGGSLVVAFEQSPV 164
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Search completed: May 13, 2005, 09:46:49
Job time : 178 secs

Result No.	Score			Match	Query	Length	DB	ID	Description
	Score	Score	Score						
1	616	72.8	127	4	US-09-513-999C-8059	Sequence 8059, Ap			
2	606.5	71.7	165	4	US-09-513-999C-7957	Sequence 7957, Ap			
3	354	31.8	86	4	US-09-513-999C-5489	Sequence 5489, Ap			
4	287	33.9	69	4	US-09-513-999C-5488	Sequence 5488, Ap			
5	242.5	28.7	146	4	US-09-248-796A-20627	Sequence 20627, A			
6	188.5	22.3	154	4	US-09-723-830-2	Sequence 2, Appli			
7	149	17.6	30	1	US-08-184-252A-5	Sequence 5, Appli			
8	149	17.6	30	5	PCT-US95-00601-5	Sequence 5, Appli			
9	124	14.7	28	4	US-09-017-689A-4	Sequence 4, Appli			
10	124	14.7	30	1	US-08-184-252A-6	Sequence 6, Appli			
11	124	14.7	30	5	PCT-US95-00601-6	Sequence 6, Appli			
12	120	14.2	350	2	US-09-123-851-3	Sequence 3, Appli			
13	120	14.2	350	2	US-08-728-520-3	Sequence 3, Appli			
14	116	13.7	350	1	US-08-184-252A-2	Sequence 2, Appli			
15	116	13.7	350	5	PCT-US95-00601-2	Sequence 2, Appli			
16	101.5	12.0	141	2	US-08-187-186A-5	Sequence 5, Appli			
17	100	11.8	123	4	US-09-248-796A-15632	Sequence 15632, A			
18	100	11.8	353	4	US-09-270-767-42030	Sequence 42030, A			
19	98.5	11.6	343	2	US-09-123-851-1	Sequence 1, Appli			
20	98.5	11.6	343	2	US-08-728-520-1	Sequence 1, Appli			
21	96.5	11.4	141	2	US-08-442-497C-9	Sequence 9, Appli			
22	96.5	11.4	141	3	US-09-333-033-9	Sequence 9, Appli			
23	96.5	11.4	141	4	US-10-004-832-9	Sequence 9, Appli			
24	96.5	11.4	157	4	US-09-949-016-7648	Sequence 7648, Ap			
25	92.5	10.9	303	4	US-09-248-796A-21504	Sequence 21504, A			
26	91	10.8	30	1	US-08-184-252A-7	Sequence 7, Appli			
27	91	10.8	30	5	PCT-US95-00601-7	Sequence 7, Appli			

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; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7957
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-7957

Query Match      71.7%; Score 606.5; DB 4; Length 165;
Best Local Similarity 71.1%; Pred. No. 5.4e-61;
Matches 118; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

Qy    1   MASGVAVSDGVIKVFNDMKVKRSTPREVKKRKKA VFCLSDDKNILLEGKEILYGDV 60
Db    1   MASGVQVADEVCRIFYDMKVCKCTPBEIKRRKKA VIFCSADKKCIIVEEGKEILYGDV 60

Qy    61  GOTVDDDPYAFVFKMLPKDKCRYALYDATTETKESKEDLVFIWFAPESAPIKSRMIYASS 120
Db    61  GVITIDPFKHFGVLMPEKDCRYALYDASFETKESRKEELMFFLWAPELAPLKSRMIYASS 120

Qy    121 KDAIKKKLTGIKHLEQLANCYEVEVDKRC TGLAFKIGGSAVISLEGKPL 166
Db    121 KDAIKKKFQGTIKHCEQANGPEDLNRA C-IAEKLGSLIVAPEGCPV 165

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RESULT 3
US-09-513-999C-5489
; Sequence 5489, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2,REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5489
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5489

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RESULT 4
US-09-513-999C-5488
; Sequence 5488, Application US/09513999C

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; Patent No. 6783961
;
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J. Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5488
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5488

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RESULT 5
US-09-248-796A-20627
; Sequence 20627, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248, 796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20627
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20627

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RESULT 6

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US-09-723-830-2
;
; Sequence 2, Application US/09723830
; Patent No. 6458930
; GENERAL INFORMATION:
; APPLICANT: Nislow, Corey
; APPLICANT: Wong, Kee
; TITLE OF INVENTION: Aspergillus fumigatus Cofilin
; FILE REFERENCE: 1039
; CURRENT APPLICATION NUMBER: US/09/723,830
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-723-830-2

Query Match      22.3%; Score 188.5; DB 4; Length 154;
Best Local Similarity 30.1%; Pred. No. 1.8e-13;
Matches 50; Conservative 34; Mismatches 57; Indels 25; Gaps 7;

QY 1 MASGVAVSDGVILKVNFMKVRKSTPEVKKRKKAVLCLSEDKNLIILBEKKEILVGDV 60
DB 3 LAGSVIADCEITAFNDFRMSGNKA-----NKTFFIIPKIADNKKRVEVID-----V 49
QY 61 GQTVDDPYATFVKML-PQKDC-----RYALYDATYET--KESKKEOLVIFFWAPESAPL 111
DB 50 SQ--EEDYEVFRSLRENTKDSKGNPAPYAVYDYLGGGEGKRSKIVFISWPSPTPT 107
QY 112 KSMIYASSKDAIKKKLTGIGIKHELQANCYEEVKORCTLAELKGGSA 157
DB 108 LWSMIYASTRENKVAL-NIHTSIHADKDGIEWTKVLAESGCKA 152

RESULT 7
US-08-184-252A-5
; Sequence 5, Application US/08184252A
; Patent No. 5573935
; GENERAL INFORMATION:
; APPLICANT: Beeler, John F.
; APPLICANT: Laroche, William
; APPLICANT: Aaronson, Stuart A.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,252A
; FILING DATE: 18-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH084.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
PCT-US95-00601-5

Query Match      17.6%; Score 149; DB 5; Length 30;
Best Local Similarity 96.7%; Pred. No. 5.3e-10;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 101 FIFWAPESAPLKSMMIYASSKDAIKKKLTG 130
DB 1 FIFWAPESAPLKSMMIYASSKDAIKKKFTG 30

RESULT 8
PCT-US95-00601-5
; Sequence 5, Application PC/TUS9500601
; GENERAL INFORMATION:
; APPLICANT: United States of America Department of Health and Human
; APPLICANT: Services
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00601
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH084.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
PCT-US95-00601-5

Query Match      17.6%; Score 149; DB 5; Length 30;
Best Local Similarity 96.7%; Pred. No. 5.3e-10;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 101 FIFWAPESAPLKSMMIYASSKDAIKKKLTG 130
DB 1 FIFWAPESAPLKSMMIYASSKDAIKKKFTG 30

RESULT 9
US-09-017-689A-4
; Sequence 4, Application US/09017689A
; Patent No. 6413940
; GENERAL INFORMATION:

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;
; APPLICANT: AVERBACK, Paul
; TITLE OF INVENTION: PHARMACEUTICALLY ACTIVE AGENTS THAT
; IMPEDE THE FORMATION OF AMYLOID BY IMPEDING THE GENESIS OF
; DMS
;
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,689A
; FILING DATE: 03-Feb-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/038,694
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 018792/0125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
;
; INFORMATION FOR SEQ ID NO: 4:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-017-689A-4
;
; Query Match 14.7%; Score 124; DB 4; Length 28;
; Best Local Similarity 96.0%; Pred. No. 3.4e-07;
; Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 46 NIIIEGKEILVGVGQTVDDPYAT 70
; Db 1 NIIIEGKDILVGVGQTVDDPYAT 25
;
; RESULT 10
; US-08-184-252A-6
; Sequence 6, Application US/08184252A
; Patent No. 5573935
;
; GENERAL INFORMATION:
; APPLICANT: Beeler, John F.
; APPLICANT: LaRoche, William
; APPLICANT: Aaronson, Stuart A.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/184,252A
; FILING DATE: 18-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH084.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
;
; US-08-184-252A-6
;
; Query Match 14.7%; Score 124; DB 1; Length 30;
; Best Local Similarity 73.3%; Pred. No. 3.7e-07;
; Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
;
; Qy 101 FIWAPESAPLKSMIYASSKDAIKKLTG 130
; Db 1 FIWAPDSAPIKSMYMTSTKDSIKKLVG 30
;
; RESULT 11
; PCT-US95-00601-6
; Sequence 6, Application PC/TUS9500601
;
; GENERAL INFORMATION:
; APPLICANT: United States of America Department of Health and Human
; APPLICANT: Services
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00601
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH084.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
;
; PCT-US95-00601-6
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; APPLICATION NUMBER: US/08/184,252A
; FILING DATE: 18-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH084.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
;
; US-08-184-252A-6
;
; Query Match 14.7%; Score 124; DB 1; Length 30;
; Best Local Similarity 73.3%; Pred. No. 3.7e-07;
; Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
;
; Qy 101 FIWAPESAPLKSMIYASSKDAIKKLTG 130
; Db 1 FIWAPDSAPIKSMYMTSTKDSIKKLVG 30
;
; RESULT 11
; PCT-US95-00601-6
; Sequence 6, Application PC/TUS9500601
;
; GENERAL INFORMATION:
; APPLICANT: United States of America Department of Health and Human
; APPLICANT: Services
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00601
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH084.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
;
; PCT-US95-00601-6
```


Query Match 14.7%; Score 124; DB 5; Length 30;
 Best Local Similarity 73.3%; Pred. No. 3.7e-07;
 Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 101 FIFWAPESAPLKSMMIYASSKDAIKKLTG 130
 Db 1 FILWAPDSAPIKSKMMYTSTKDSIRKLVG 30

RESULT 12

US-09-123-851-3
 ; Sequence 3, Application US/09123851
 ; Patent No. 5958405
 ; GENERAL INFORMATION:
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09123,851
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/728,520
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0136 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 350 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 451482

US-09-123-851-3
 Query Match 14.2%; Score 120; DB 2; Length 350;
 Best Local Similarity 27.0%; Pred. No. 3.6e-05;
 Matches 34; Conservative 36; Mismatches 40; Indels 16; Gaps 6;

QY 27 BEVKRRKKAFLCLSEDKKNILE---EGKEILVGVGQ---TVDDPYATFV-KMLPKDK 79
 Db 11 EDVKE-----IFARANGKRYLLKISIEQVLVIGSYQSPDSWDKYDSFVLPLEDKQ 65

QY 80 CRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASSKDAIKKLTG--IKHELOA 137
 Db 66 PCYILF--RLDSQNAQGYEWIFIAWSPDHSVRQKMLYAATRAATLKKEFGGHIKDEVFG 123

QY 138 NCYEEV 143

Db 124 TVKEDV 129

RESULT 13

US-08-728-520-3
 ; Sequence 3, Application US/08728520
 ; Patent No. 5994112
 ; GENERAL INFORMATION:
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/728,520
 FILING DATE: Filed Herewith
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0136 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 350 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 451482

US-08-728-520-3
 Query Match 14.2%; Score 120; DB 2; Length 350;
 Best Local Similarity 27.0%; Pred. No. 3.6e-05;
 Matches 34; Conservative 36; Mismatches 40; Indels 16; Gaps 6;

QY 27 BEVKRRKKAFLCLSEDKKNILE---EGKEILVGVGQ---TVDDPYATFV-KMLPKDK 79
 Db 11 EDVKE-----IFARANGKRYLLKISIEQVLVIGSYQSPDSWDKYDSFVLPLEDKQ 65

QY 80 CRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASSKDAIKKLTG--IKHELOA 137
 Db 66 PCYILF--RLDSQNAQGYEWIFIAWSPDHSVRQKMLYAATRAATLKKEFGGHIKDEVFG 123

QY 138 NCYEEV 143

Db 124 TVKEDV 129

RESULT 14

US-08-184-252A-2
 ; Sequence 2, Application US/08184252A
 ; Patent No. 5573935
 ; GENERAL INFORMATION:
 ; APPLICANT: Beeler, John F.
 ; APPLICANT: LaRoche, William
 ; APPLICANT: Aaronson, Stuart A.
 ; TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe, Martens Olson & Bear

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 13, 2005, 09:44:01 ; Search time 116.5 Seconds
(without alignments)
3326.471 Million cell updates/sec

Title: US-10-649-952A-2

Perfect score: 901

Sequence: 1 atggctccggtgtggtgtg.....tggaggcgaagcctttgtga 501

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=A_Geneseq -QMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10649952 @CGN 1.1.224 @runat_13052005_102648_27307 -NCPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq 16Dec04:*

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2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	846	93.9	166	5	ABBB1882
2	846	93.9	166	6	ADA37012
3	846	93.9	166	8	ADI24535
4	846	93.9	166	8	ADO05889
5	846	93.9	166	8	ADQ30534
6	846	93.9	229	8	ADO65133
7	842	93.5	187	6	ABR41637
8	841	93.3	239	8	ADN99790
9	764	84.8	149	7	ADJ70464
10	702	77.9	166	6	ABR41956

11	699	77.6	166	4	AAM78545	Aam78545 Human pro
12	699	77.6	166	7	ADB75248	ADB75248 Prostate
13	699	77.6	166	7	ADJ70104	Adj70104 Human hea
14	699	77.6	166	8	ADI24536	ADI24536 Human mod
15	699	77.6	205	4	AAU18546	Aau18546 Human cyt
16	699	77.6	207	4	AAM79529	Aam79529 Human pro
17	666.5	74.0	154	8	ADN99460	Adn99460 Novel hum
18	645.5	71.6	153	8	ADN99430	Adn99430 Novel hum
19	628	69.7	127	3	AAG03978	Ag03978 Human sec
20	606.5	67.3	165	3	AGG03876	Ag03876 Human sec
21	606.5	67.3	165	4	AAM40267	Aam40267 Human pol
22	606.5	67.3	165	8	ADI24537	ADI24537 Human mod
23	606.5	67.3	165	8	ADQ30570	Adq30570 Pancreas
24	606.5	67.3	165	8	ADP23096	Adp23096 PRO polyp
25	606.5	67.3	188	4	AAM42053	Aam42053 Human pol
26	581.5	64.5	170	8	ADI24538	ADI24538 Human mod
27	562.5	62.4	180	8	ADI24539	ADI24539 Human mod
28	557.5	61.9	148	7	ADJ70545	Adj70545 Human hea
29	520.5	57.8	111	7	ADE15627	Ade15627 Human str
30	460	51.1	129	4	AAU18547	Aau18547 Human cyt
31	450	49.9	156	4	AAU18521	Aau18521 Human cyt
32	426	47.3	144	8	ADI24541	ADI24541 Human mod
33	402.5	44.7	131	8	ADP30110	Adp30110 Human sec
34	401.5	44.6	136	8	ADI24540	ADI24540 Human mod
35	393.5	43.7	106	8	ADN99385	Adn99385 Novel hum
36	390	43.3	110	8	ADN99316	Adn99316 Novel hum
37	390	43.3	110	8	ADP30004	Adp30004 Human sec
38	374	41.5	209	4	ABG20129	Abg20129 Novel hum
39	354	39.3	86	3	AGG01408	Agg01408 Human sec
40	287	31.9	69	3	AAU01407	Aau01407 Human sec
41	273	30.3	106	5	ABP43208	Abp43208 Human ova
42	267.5	29.7	143	8	ADS43863	Ads43863 Bacterial
43	253.5	28.1	141	8	ADN12253	Adn12253 C. albica
44	245.5	27.2	141	8	ADN12255	Adn12255 C. albica
45	230	25.5	60	8	ABO56473	Abo56473 Human gen

ALIGNMENTS

RESULT 1

ABBB1882
ID ABBB1882 standard; protein; 166 AA.
XX

AC ABBB1882;

DT 23-SEP-2002 (first entry)

XX Human coflin 1 (non-muscle).

DE Human coflin 1 (non-muscle).

XX Human; coflin 1; CFL1; gene therapy; antisense gene therapy;

KW immunological disorder.

XX Homo sapiens.

OS WO200194376-A1.

PN 13-DEC-2001.

PD 11-JUN-2001; 2001WO-US018815.

PF 09-JUN-2000; 2000US-0210884P.

PR (GENA-) GENAISSANCE PHARM INC.

XX Anastasio AE, Duda A, Klien SE, Koshy B, Sausker EA;

XX WPI; 2002-566437/60.

DR N-PSDB; ABQ88640, ABQ88641.

XX Novel genetic variants of human coflin 1, CFL1 gene for studying

PT expression, function of the gene and expressing CFL1 protein useful in

PT identifying drugs to treat immunological disorders.

XX

PS Disclosure: Fig 3; 84pp; English.

XX The invention relates to a novel polynucleotide sequence which is a
 CC polymorphic variant of a reference sequence for the cofillin 1 (non-
 CC muscle) (CFL1) gene or its fragment, or a polymorphic variant of a
 CC reference sequence for a CFL1 cDNA or its fragment. The polynucleotide of
 CC the invention may have a use in gene therapy, and in antisense gene
 CC therapy. The polynucleotide is useful for studying the expression and
 CC function of CFL1 and expressing CFL1 protein for use in screening for
 CC candidate drugs to treat diseases related to CFL1 activity. The
 CC polymorphism and haplotype data are useful for validating whether CFL1 is
 CC a suitable target for drugs to treat immunological disorders, screening
 CC for such drugs and reducing bias in clinical trials of such drugs. The
 CC present sequence represents the human cofillin 1 (non-muscle) of the
 CC invention

XX Sequence 166 AA;

Alignment Scores:
 Pred. No.: 1,43e-82 Length: 166
 Score: 846.00 Matches: 166
 Percent Similarity: 100.00% Conservativeness: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.90% Indels: 0
 DB: 5 Gaps: 0

US-10-649-952A-2 (1-501) x ABB81882 (1-166)

Qy 1 ATGCGCTCCGGTGGCTGCTCTGATGTTCAAGGTTTCAACGACATGAAGTG 60
 Db 1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20
 Qy 61 CGTAAGCTTCAACGCCAGAGGAGTGTAGAGGCGGAGAGGCGGCTCTCTCGCTG 120
 Db 21 ArgLysSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
 Qy 121 AGTGAGGACAAAGAAACATCATCTCTGAGGAGGCGGAGAGATCTCTGGGCGATGTG 180
 Db 41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
 Qy 181 GGCAGAGTGTGAGAGTCTCTAGCCACCTTTGTCAAGATGCTGCCAGATAAGGATGC 240
 Db 61 GlyGlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCys 80
 Qy 241 CGCTATGCTCTATGATGCAACCTATGACACCAAGAGGAGGAGGAGGAGGATCTCGTG 300
 Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
 Qy 301 TTTATCTTCTGGGCCCCGAGTCTGCGCCCCCTTAAGAGCAAAATGATTTATGCCAGCTCC 360
 Db 101 PheIlePheThrAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
 Qy 361 AAGGAGCCATCAAGAGAAGCTGACAGGAGTCAAGGATCAAGCATGAATTGCAAGCAAACTGTAC 420
 Db 121 LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyr 140
 Qy 421 GAGGAGTCAAGGACCCCTGACCTGGCAGAGAGCTGGGGGACGTGGCTCATCTCC 480
 Db 141 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer 160
 Qy 481 CTGGAGGCGCAAGCCTTTG 498
 Db 161 LeuGluGlyLysProLeu 166

RESULT 2

ADA37012
 ID ADA37012 standard; protein; 166 AA.

XX ADA37012;

AC 20-NOV-2003 (first entry)

DT Human cofillin protein SEQ ID NO:1.

XX

XX proliferation; differentiation; haematopoietic stem cell; cofillin;
 KW vasotrophic; antianemic; cytostatic; vulnary; nephrotropic;
 KW hepatotropic; haematopoietic hypofunction; Fanconi's disease;
 KW malignant lymphoma; acute leukaemia; chronic hepatic obstruction;
 KW kidney failure; surgical trauma; transfusion trauma; infection;
 KW snakebite; haemorrhagic uraemia; splenomegaly; Barnard-Soulier disease;
 KW Glanzmann's thrombasthenia; idiopathic thrombocytopenic purpura; human.
 XX Homo sapiens.
 OS
 XX WO2003057241-A1.
 PN
 XX 17-JUL-2003.
 PD
 XX 27-DEC-2002; 2002WO-JP013862.
 PF
 XX 28-DEC-2001; 2001JP-00400330.
 PR
 XX (DAII-) DAIICHI SUNTORY PHARMA CO LTD.
 PA (SUNR) SUNTORY LTD.
 PA (DAII-) DAIICHI SUNTORY BIOMEDICAL RES LTD.
 XX
 PI Miura K, Haruyama M, Kodama S;
 XX
 DR WPI: 2003-587077/55.
 DR N-PSDB; ADA37013.
 XX
 PT Agents containing cofillin promoting proliferation and differentiation of
 PT haematopoietic stem cells and their precursors for treatment of
 PT haematopoietic deficiency diseases.
 XX
 PS Claim 2; Fig 1; 57pp; Japanese.
 CC
 CC The present invention describes agents (A) promoting the proliferation
 CC and/or differentiation of haematopoietic stem cells and/or their
 CC precursor cells. (A) contain cofillin or a peptide of similar activity as
 CC active component. Also described: (1) promoting the proliferation and/or
 CC differentiation of haematopoietic stem cells and/or their precursor
 CC cells, using (A); and (2) treating diseases associated with
 CC haematopoietic cell deficiency, using (A). (A) have vasotrophic,
 CC antianemic, cytostatic, vulnary, nephrotropic and hepatotropic
 CC activities. (A) can be used for treating and preventing diseases
 CC associated with a diffuse decrease in haematopoietic cell numbers and/or
 CC haematopoietic hypofunction, such as Fanconi's disease, malignant
 CC lymphoma, acute leukaemia, chronic hepatic obstruction, kidney failure,
 CC surgical or transfusion trauma, serious infections, snakebite,
 CC haemorrhagic uraemia, splenomegaly, Barnard-Soulier disease, Glanzmann's
 CC thrombasthenia, and idiopathic thrombocytopenic purpura. The present
 CC sequence represents human cofillin, which is given in the exemplification
 CC of the present invention.

SQ Sequence 166 AA;

Alignment Scores:
 Pred. No.: 1,43e-82 Length: 166
 Score: 846.00 Matches: 166
 Percent Similarity: 100.00% Conservativeness: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.90% Indels: 0
 DB: 6 Gaps: 0

US-10-649-952A-2 (1-501) x ADA37012 (1-166)

Qy 1 ATGCGCTCCGGTGGCTGCTCTGATGTTCAAGGTTTCAACGACATGAAGTG 60
 Db 1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20
 Qy 61 CGTAAGCTTCAACGCCAGAGGAGTGTAGAGGCGGAGAGGCGGCTCTCTCGCTG 120
 Db 21 ArgLysSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
 Qy 121 AGTGAGGACAAAGAAACATCATCTCTGAGGAGGCGGAGAGATCTCTGGGCGATGTG 180

PD 29-APR-2004.
XX
PF 15-OCT-2003; 2003WO-GB004450.
XX
PR 15-OCT-2002; 2002GB-00024014.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (FARB) BAYER HEALTHCARE AG.
XX
XX Bacon KB, Herath HMC, Liu N, Rohlff C;
XX WPI; 2004-348336/32.
DR N-PSDB; ADO05890.
XX
XX Treating or preventing an inflammatory disease, e.g., asthma comprises
PT administering to a subject an agonist or antagonist of cofilin isoform 1
PT or 2 that modulates the expression or activity of a cofilin polypeptide.
XX
XX Claim 6; SEQ ID NO 1; 47pp; English.
XX
CC The invention relates to treating or preventing an inflammatory disease
CC and involves administering to a subject, an agent that modulates the
CC expression or activity of a cofilin polypeptide. The agent is an agonist
CC or antagonist of cofilin isoform 1 or 2. Antiasthmatic. The method is
CC useful in treating or preventing an inflammatory disease, e.g., asthma.
CC The present sequence represents a human cofilin polypeptide.
XX
SQ Sequence 166 AA;

Alignment Scores:
Pred. No.: 1.43e-82 Length: 166
Score: 846.00 Matches: 166
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.90% Indels: 0
DB: 8 Gaps: 0

US-10-649-952A-2 (1-501) x ADO05889 (1-166)
Qy 1 ATGCCCTCCGGTGGCTGCTCTGATGGTGTATCAAGGTGTTCAACGACATGAAGTG 60
Db 1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20
Qy 61 CGTAAGTCTTCAACGCCAGAGGAGGTGAGAGGCGCAAGAGCGGCTCTCTGCTG 120
Db 21 ArgLysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
Qy 121 AGTGAGGACAGAAAGAACATCATCTGAGGAGGCGCAAGAGATCTCTGGGCGATGTG 180
Db 41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
Qy 181 GGCAGAGCTGCGAGATCCCTACGCCACCTTTCTCAAGATGCTGCCAGATAAGATGTC 240
Db 61 GlyGlnThrValAspAspProTyAlaThrPheValLysMetLeuProAspLysAspCys 80
Qy 241 CGCTATCCCTCTATGATGCACCTATGACACCAAGGAGGAGGAGGAGGAGGATCTGCTG 300
Db 81 ArgTyAlaLeuTyAlaThrTyAlaThrTyAlaThrTyAlaThrTyAlaThrTyAlaThr 100
Qy 301 TTTATCTTCTGGGCCCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCCAGCTCC 360
Db 101 PheIlePheThrAlaProGluSerAlaProLeuLysSerLysMetIleTyAlaSerSer 120
Qy 361 AAGACGCCATCAAGAGAAGCTGACAGGATCAAGGATCAAGATGATGCAAGCAAACTGTAC 420
Db 121 LysAspAlaIleLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTy 140
Qy 421 GAGGAGCTCAGGACCCCTGACCTGCGAGAGAGCTGGGGGCGAGTGGGCTCATCTCC 480
Db 141 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer 160
Qy 481 CTGGAGGCGCAAGCCTTTG 498

Db 161 LeuGluGlyLysProLeu 166
RESULT 5
ADQ30534
ID ADQ30534 standard; protein; 166 AA.
XX
AC ADQ30534;
XX
DT 23-SEP-2004 (first entry)
XX
XX Pancreas cancer marker - non-muscle cofilin isoform.
XX cytostatic; diagnosis; pancreatic cancer; antibody; antisense construct;
XX differential expression.
XX Homo sapiens.
XX WO2004055519-A2.
XX
XX 01-JUL-2004.
XX
XX 11-DEC-2003; 2003WO-EP014057.
XX
XX 17-DEC-2002; 2002EP-00028058.
PR 05-NOV-2003; 2003EP-00025237.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.
XX
XX Chen J, Hu L, Liu TH, Lu ZH, Shen Y;
XX WPI; 2004-488121/46.
XX
XX New specific markers comprises at least one polypeptide up-regulated in
PT pancreatic cancer, useful for diagnosing pancreatic cancer.
XX
XX Claim 1; SEQ ID NO 21; 381pp; English.
XX
CC The invention relates to a marker (I) for diagnosis of pancreatic cancer
CC comprising at least one polypeptide selected from 55 proteins up-
CC regulated in pancreatic cancer (Table 2 and Table 3, given in the
CC specification) or from 68 proteins with higher levels in pancreatic
CC cancer compared to normal tissue (Table 6, given in the specification).
CC (I) is a polypeptide for use as a marker or as a component of a marker
CC for diagnosis of pancreatic cancer and/or the susceptibility to
CC pancreatic cancer. A compound (antibody, an antibody-derivative, an
CC antibody fragment, a peptide, or an antisense construct) identified by
CC screening methods using (I) is useful for the treatment or prevention of
CC pancreatic cancer. It is also useful for the preparation of a diagnostic
CC composition for diagnosing pancreatic cancer or a predisposition for
CC pancreatic cancer. The current polypeptides were found to be
CC differentially expressed in pancreatic tissue obtained from individuals
CC suffering from pancreatic cancer as compared to healthy pancreatic
CC tissue. They have been identified as suitable as markers of pancreatic
CC cancer for early diagnosis of the disease. This sequence corresponds to a
CC protein marker of the invention.
XX
SQ Sequence 166 AA;

Alignment Scores:
Pred. No.: 1.43e-82 Length: 166
Score: 846.00 Matches: 166
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.90% Indels: 0
DB: 8 Gaps: 0

US-10-649-952A-2 (1-501) x ADQ30534 (1-166)
Qy 1 ATGCCCTCCGGTGGCTGCTCTGATGGTGTATCAAGGTGTTCAACGACATGAAGTG 60
Db 1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20

QY 61 CGTAAGTCTTCAAGCCAGAGGAGGTGAAGAGCGCAAGAGCGGTGCTCTTCTGCTG 120
 Db 21 ArgLysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
 QY 121 AGTGAGCAAGAGCAATCATCTGAGGAGGCAAGAGATCTCTGTTGGCGATGTG 180
 Db 41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
 QY 181 GGCCAGACTGTCAGCATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
 Db 61 GlyGlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCys 80
 QY 241 CGCTATGCCCTCTATGATGCAACTATGAGACCAAGAGAGCAAGAGAGGATCTGGTG 300
 Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
 QY 301 TTTATCTTCTGGCCCGAGTCTGGCCCTTAAAGAGCAAAATGATTATGACGCTCC 360
 Db 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
 QY 361 AAGGAGCCCATCAAGAGAGCTGACAGGAGTCAAGCATGAATTGCAAGCAAACTGCTAC 420
 Db 121 LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyr 140
 QY 421 GAGGAGTCAAGGACCGCTGCACCTGCGAGAGAGCTGGGGGCGAGTGGGTCATCTCC 480
 Db 141 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer 160
 QY 481 CTGGAGGGCAAGCCTTTG 498
 Db 161 LeuGluGlyLysProLeu 166

RESULT 6
 ADQ65133
 ID ADQ65133 standard; protein; 229 AA.
 XX
 AC ADQ65133;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Novel human protein sequence #106.
 XX
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KW gene therapy; diagnostic marker; morbid state; osteoporosis;
 KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN EP1440981-A2.
 XX
 PD 28-JUL-2004.
 XX
 PF 21-JAN-2004; 2004BP-00001196.
 XX
 PR 21-JAN-2003; 2003JP-00102206.
 XX
 PR 09-MAY-2003; 2003JP-00131392.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Nagai K, Irie R;
 XX
 DR WPI: 2004-535376/52.
 DR N-PSDB; ADQ62945.
 XX
 XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 XX
 PS Claim 1; SEQ ID NO 2294; 2449pp; English.
 XX
 CC The invention relates to 2495 novel polynucleotides (1) and their encoded
 CC polypeptides, sequences hybridizing to these nucleotides, sequences

CC encoding partial polypeptides and sequences having 70% or 90% identity to
 CC the nucleotide and protein sequences. The nucleotides and polypeptides
 CC are useful as diagnostic markers or therapeutic target for the diseases
 CC or morbid states. They are also useful for treating osteoporosis,
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
 CC dementia and various cancers. This sequence corresponds to a protein
 XX sequence of the invention.
 SQ Sequence 229 AA;
 Alignment Scores:
 Pred. No.: 1.58e-82 Length: 229
 Score: 846.00 Matches: 166
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.90% Indels: 0
 DB: 8 Gaps: 0
 US-10-649-952A-2 (1-501) x ADQ65133 (1-229)
 QY 1 ATGGCCTCCGGTGTGGCTGCTCTGATGTGTCTCATCAAGGTGTTCAACGACATGAGGTG 60
 Db 64 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 83
 QY 61 CGTAAGTCTTCAACGCCAGAGGAGGTGAAGAGCGCAAGAGCGGTGCTCTTCTGCTG 120
 Db 84 ArgLysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 103
 QY 121 AGTGAGCAAGAGCAATCATCTGAGGAGGCGCAAGAGATCTCTGTTGGCGATGTG 180
 Db 104 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 123
 QY 181 GGCCAGACTGTCAGCATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
 Db 124 GlyGlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCys 143
 QY 241 CGCTATGCCCTCTATGATGCAACCTATGAGACCAAGGAGAGCAAGAGGAGGATCTGGTG 300
 Db 144 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 163
 QY 301 TTTATCTTCTGGCCCCCGAGTCTGGCCCCCTTAAGAGCAAAATGATTATTCAGACTCC 360
 Db 164 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 183
 QY 361 AAGGAGCCCATCAAGAGAGCTGACAGGAGTCAAGCATGATTCGACCAAGCAACTGCTAC 420
 Db 184 LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyr 203
 QY 421 GAGGAGGTCAAGGACCGCTGCACCTCGCAGAGAGTGGGGGCGAGTGGCGTCATCTCC 480
 Db 204 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlySerAlaValIleSer 223
 QY 481 CTGGAGGGCAAGCCTTTG 498
 Db 224 LeuGluGlyLysProLeu 229

RESULT 7
 ABR41637
 ID ABR41637 standard; protein; 187 AA.
 XX
 AC ABR41637;
 XX
 DT 02-JUN-2003 (first entry)
 XX
 DE Human DITHP cytoskeletal protein.
 XX
 KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
 KW cancer; cell proliferative disorder; autoimmune disorder;
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 KW neurological disorder; gastrointestinal disorder; transport disorder;
 KW connective tissue disorder; drug screening; proteome analysis;
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
 KW disease model; toxicological testing; transcript imaging;

KW cytoskeletal protein.

OS Homo sapiens.

XX WO200297031-A2.

XX 05-DEC-2002.

XX 27-MAR-2002; 2002WO-US010056.

XX 28-MAR-2001; 2001US-0279619P.

XX 29-MAR-2001; 2001US-0280067P.

XX 29-MAR-2001; 2001US-0280068P.

XX 16-MAY-2001; 2001US-0291280P.

XX 17-MAY-2001; 2001US-0291829P.

XX 17-MAY-2001; 2001US-0291849P.

XX 19-JUN-2001; 2001US-0299428P.

XX 20-JUN-2001; 2001US-0299776P.

XX 20-JUN-2001; 2001US-0300001P.

XX (INCYTE GENOMICS INC.

XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;

XX DuFour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;

XX Daugherty SC, Dam TC, Liu TP, Nguyen DA, Kleefeld Y, Gerstin EH;

XX Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;

XX Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX WPI; 2003-129518/12.

XX N-PSDB; ACC46574.

XX Novel human diagnostic and therapeutic polypeptide useful for identifying

XX test compound which specifically binds to a polypeptide encoded by human

XX diagnostic and therapeutic polynucleotide, and to induce antibodies.

XX Claim 27; SEQ ID NO 1172; 591pp; English.

XX The invention relates to novel human diagnostic and therapeutic

XX polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded

XX proteins (DITHP; ABR41136-ABR41812). The invention also relates to

XX polynucleotide sequences at least 90% identical to the dithp cDNA

XX sequences of the invention; recombinant vectors, host cells and

XX transgenic organisms comprising a dithp nucleic acid sequence; the

XX recombinant production of DITHP proteins; antibodies specific for DITHP

XX proteins; microarrays comprising dithp nucleic acid sequences; methods of

XX detecting dithp nucleotide and protein sequences; methods of screening

XX for compounds which specifically bind a DITHP protein; and methods of

XX assessing the toxicity of test compounds using a dithp hybridisation

XX probe. Dithp nucleic acid sequences and DITHP proteins may be used in the

XX diagnosis of a wide variety of conditions including cancer and other cell

XX proliferative disorders; autoimmune or inflammatory disorders; bacterial,

XX viral, fungal or parasitic infections; hormonal disorders; metabolic

XX disorders; neurological disorders; gastrointestinal disorders; transport
XX disorders; and connective tissue disorders. They may also be used to
XX screen for modulators of protein activity or gene expression. DITHP
XX proteins can additionally be used in analysis of the proteome of a tissue
XX or cell type and to induce antibodies. The dithp nucleic acids are
XX additionally useful in somatic or germline gene therapy of the disorders
XX mentioned above, as a source of antisense sequences, as a source of
XX probes and primers, in genotyping and identification of individuals, in
XX the generation of transgenic animal models of human disease or knock in
XX humanised animals, in toxicological testing, and in transcript imaging.
XX The present sequence represents a DITHP protein which is a cytoskeletal
XX protein. Note: the sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 187 AA;

XX Alignment Scores:

XX Pred. No.: 4.03e-82 Length: 187

XX Score: 842.00 Matches: 165

XX Percent Similarity: 99.40% Conservative: 0

Best Local Similarity:	99.40%	Mismatches:	1
Query Match:	93.45%	Indels:	0
DB:	6	Gaps:	0
US-10-649-952A-2 (1-501) x ABR41637 (1-187)			
Qy	1	ATGGCCTCCGGTGTGGCTGTCTCTGATGGTTCATCAAGGTGTTCACACGACATGAAGGTG	60
Db	22	MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal	41
Qy	61	CGTAAGTCTTCAAGCCGACAGAGAGGTGTAAGAGCGCAAGAGCGGCTCTTCTGCTG	120
Db	42	ArgLysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu	61
Qy	121	AGTGAGGACAAGAAGAACATCATCTCGAGGAGGCAAGAGAGATCCTGGTGGGCGCATGTG	180
Db	62	SerGluAspLysLysAsnIleIleLeuGluGluGlyLysGluIleLeuValGlyAspVal	81
Qy	181	GGCCAGACTGTGACGATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC	240
Db	82	GlyGlnThrValAspAspProTyrThrThrPheValLysMetLeuProAspLysAspCys	101
Qy	241	CGCTATGCCCTCTATGATGCAACCTATGACACCAAGAGAGCAAGAGGAGGATCTGGTG	300
Db	102	ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal	121
Qy	301	TTTATCTTCGGGCCCCCGAGTCTGGCCCTTTAAGAGCAAAATGATTATGCCAGCTCC	360
Db	122	PheIlePheThrAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer	141
Qy	361	AAGGACGCCATCAAGAGAAGCTGCACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC	420
Db	142	LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyr	161
Qy	421	GAGAGGTCAAGGACCGCTCCACCCCTGGCAGAGAGCTGGGGGGCAGTGGCGTCATCTCC	480
Db	162	GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer	181
Qy	481	CTGGAGGCGAAGCCTTTG 498	
Db	182	LeuGluGlyLysProLeu 187	
RESULT 8			
ADN99790			
ID	ADN99790	standard; protein; 239 AA.	
XX	AC	ADN99790;	
XX	DT	29-JUL-2004 (first entry)	
XX	DE	Novel human protein sequence #606.	
XX	KW	anti-inflammatory; dermatological; neuroprotective; immunomodulator;	
XX	KW	antibacterial; virucide; antipsoriatic; cytostatic; gene therapy;	
XX	KW	vaccine; inflammatory; CNS; immune disorder; cancer; psoriasis; diabetes;	
XX	KW	early aging; hormonal imbalance; ischemic heart disease;	
XX	KW	ulcerative colitis.	
OS	Homo sapiens.		
XX	WO2004038003-A2.		
XX	06-MAY-2004.		
XX	24-OCT-2003; 2003WO-US033947.		
XX	25-OCT-2002; 2002US-0421061P.		
XX	25-OCT-2002; 2002US-0421080P.		
XX	25-OCT-2002; 2002US-0421552P.		
XX	25-OCT-2002; 2002US-0421614P.		
XX	30-OCT-2002; 2002US-0422177P.		
XX	30-OCT-2002; 2002US-0422178P.		
XX	15-NOV-2002; 2002US-0426355P.		

PR 15-NOV-2002; 2002US-0426384P.
 PR 15-NOV-2002; 2002US-0426394P.
 PR 15-NOV-2002; 2002US-0426430P.
 PR 15-NOV-2002; 2002US-0426916P.
 PR 27-NOV-2002; 2002US-0429224P.
 PR 27-NOV-2002; 2002US-0429275P.
 PR 27-NOV-2002; 2002US-0429302P.
 PR 27-NOV-2002; 2002US-0429326P.
 PR 27-NOV-2002; 2002US-0429651P.
 PR 04-DEC-2002; 2002US-0430645P.
 PR 04-DEC-2002; 2002US-0430651P.
 PR 04-DEC-2002; 2002US-0430657P.
 PR 04-DEC-2002; 2002US-0430663P.
 PR 04-DEC-2002; 2002US-0430688P.
 PR 04-DEC-2002; 2002US-0430684P.
 PR 05-DEC-2002; 2002US-0430937P.
 PR 05-DEC-2002; 2002US-0430965P.
 PR 05-DEC-2002; 2002US-0431458P.
 PR 12-DEC-2002; 2002US-0433251P.
 PR 12-DEC-2002; 2002US-0433500P.
 PR 13-DEC-2002; 2002US-0433316P.
 PR 13-DEC-2002; 2002US-0433318P.
 PR 23-DEC-2002; 2002US-0436236P.
 PR 03-JAN-2003; 2003US-0437914P.
 PR 17-JAN-2003; 2003US-0440820P.
 PR 17-JAN-2003; 2003US-0440821P.
 PR 18-APR-2003; 2003US-0463700P.
 PR 18-APR-2003; 2003US-0463708P.
 PR 18-APR-2003; 2003US-0463716P.
 PR 18-APR-2003; 2003US-0463732P.
 PR 02-MAY-2003; 2003US-0467199P.
 PR 02-MAY-2003; 2003US-0467201P.
 PR 02-MAY-2003; 2003US-0467203P.
 PR 02-MAY-2003; 2003US-0467230P.
 PR 15-MAY-2003; 2003US-0471306P.
 PR 15-MAY-2003; 2003US-0471336P.
 PR 22-MAY-2003; 2003US-0472420P.
 PR 22-MAY-2003; 2003US-0472430P.
 PR 09-JUN-2003; 2003US-0476609P.
 PR 09-JUN-2003; 2003US-0476621P.
 PR 09-JUN-2003; 2003US-0476632P.
 PR 09-JUN-2003; 2003US-0476841P.
 PR 08-JUL-2003; 2003US-0485217P.
 PR 08-JUL-2003; 2003US-0485218P.
 PR 08-JUL-2003; 2003US-0485223P.
 PR 08-JUL-2003; 2003US-0485224P.
 PR 08-JUL-2003; 2003US-0485325P.
 PR 08-JUL-2003; 2003US-0485359P.
 PR 14-JUL-2003; 2003US-0486446P.
 PR 14-JUL-2003; 2003US-0486480P.
 PR 15-JUL-2003; 2003US-0486891P.
 PR 15-JUL-2003; 2003US-0486960P.
 PR 08-AUG-2003; 2003US-0493341P.
 PR 08-AUG-2003; 2003US-0493370P.
 PR 08-AUG-2003; 2003US-0493573P.
 PR 08-AUG-2003; 2003US-0493577P.
 XX
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
 PI Halenbeck RF, Kothakota S, Lin H, Linnemann T, Pierce K, Wang Y;
 PI Wong JGP, Wu G, Zhang H, Zeng C;
 XX WPI; 2004-365511/34.
 DR N-PSDB; ADN99006.
 XX
 PT New nucleic acid molecules, useful in preparing a composition for
 PT treating or preventing e.g. inflammatory, CNS, bacterial or viral
 PT disorders, cancer, psoriasis, diabetes, ischemic heart disease or
 PT ulcerative colitis.
 XX
 PS Claim 14; SEQ ID NO 1390; 532pp; English.
 XX

CC The invention relates to a nucleic acid molecule comprising a
 CC polynucleotide sequence or its complement that encodes a polypeptide. The
 CC nucleic acid is useful in preparing a composition for treating or
 CC preventing inflammatory, CNS, immune, bacterial or viral disorder,
 CC cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic
 CC heart disease or ulcerative colitis. This sequence corresponds to a
 CC protein of the invention.
 XX
 SQ Sequence 239 AA;
 Alignment Scores:
 Pred. No.: 5,6e-82 Length: 239
 Score: 841.00 Matches: 165
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.34% Indels: 0
 DB: 8 Gaps: 0
 US-10-649-952A-2 (1-501) x ADN99790 (1-239)
 QY 4 GCCTCCGGTGTGGCTCTCTCTGATGTGTCATCAAGGTGTTCACGACATGAAGTGCCT 63
 Db 75 AlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysValArg 94
 QY 64 AGTCTTCAACGCCAGAGGAGGTGAAGAGCGCAAGAGCGGTGCTCTTCCTCGCTAGT 123
 Db 95 LysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeuSer 114
 QY 124 GAGGACAAGAACATCATCTCTGGAGGAGGCGCAGGAGATCTGCTGGCGATGTGGGC 183
 Db 115 GluAspLysLysAsnIleIleLeuGluGluGlyLysGluIleLeuValGlyAspValGly 134
 QY 184 CAGACTGTGCGAGGATCCCTACGCCACTTTGTCAAGATGCTGCAGATAAGGACTGCCGC 243
 Db 135 GlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCysArg 154
 QY 244 TATGCCCTCTATGATGCAACCTATGAGACCAAGGAGAGCAAGAGAGGATCTGTGTTT 303
 Db 155 TyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuValPhe 174
 QY 304 ATCTTCTGGGCCCCGAGTCTGCGCCCTTAGAGCAAAATGATTTATGCCAGCTCCAAG 363
 Db 175 IlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSerLys 194
 QY 364 GACGCCATCAAGAAGAGCTGACAGGATCAAGCATGAATTGCAAGCAAACTCTACGAG 423
 Db 195 AspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyrGlu 214
 QY 424 GAGGTCAAGGACCGTGCACCTGCGCAGAGAAGTGGGGGCGAGTCCGGTCAATCTCCCTG 483
 Db 215 GluValLysAspArgCysThrLeuAlaGluLysLeuGlySerAlaValIleSerLeu 234
 QY 484 GAGGCGACGCTTTG 498
 Db 235 GluGlyLysProLeu 239
 RESULT 9
 ADJ70464
 ID ADJ70464 standard; protein; 149 AA.
 XX
 AC ADJ70464;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human heat mitochondrial protein as a therapeutic target SeqID2270.
 XX
 KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.

US-10-649-952A-2 (1-501) x ABR1956 (1-166)

QY 1 ATGCGCTCCGGTGTGGTGTCCTCTCATAGGTGTCAACGACATGAAGTGC 60
DB 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20

QY 61 CGTAAGTCTTCAAGCCAGGAGGTGAGAACGCCGAAGAGCGGGTGTCTTCGCTGC 120
DB 21 ArgLysSerSerThrGlnGluGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40

QY 121 AGTGAGGACAAGAACAATCATCTCTGGAGGAGGCGCAAGAGATCTGTGGCGCATGTG 180
DB 41 SerAspAspLysArgGlnIleValGluGluAlaLysGlnIleLysAlaValLeuPheCysLeu 100

QY 181 GCGCAGACTGTCAGCATCCCTTACGACATGCTGCTGCAAGATGCTGCCAGATAAGACTGC 240
DB 61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 80

QY 241 CGCTATGCCCTCTATGATGCAACCTATGAGACCAAGAGAGCAAGAGAGGATCTGGTG 300
DB 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100

QY 301 TTTATCTTCTGGCCCCCGAGTCTGCGCCCTTAAGACAAATGATTATTCAGCTCC 360
DB 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120

QY 361 AAGGACGCCATCAAGAAGAAGCTGACAGGATCAAGCATGAATTCGAAGCAAACCTGCTAC 420
DB 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 140

QY 421 GAGGAGGTCAAGGACCGCTGACCCTGCGAGAGAGTGGGGGCGAGTGGCGGTCTATCTCC 480
DB 141 AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyGlyAsnValValIleSer 160

QY 481 CTGGAGGGCAAGCCTTTTG 498
DB 161 LeuGluGlyLysProLeu 166

RESULT 11
ID AAM78545
XX AAM78545 standard; protein; 166 AA.
AC AAM78545;
XX XX
DT 06-NOV-2001 (first entry)
DE Human protein SEQ ID NO 1207.
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.

OS Homo sapiens.
XX XX
PN WO200157190-A2.
XX XX
PD 09-AUG-2001.
XX XX
PF 05-FEB-2001; 2001WO-US004098.
XX XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX XX
PA (HYSE-) HYSEQ INC.
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
WPI: 2001-476283/51.
N-PSDB; AAKS1678.
Nucleic acids encoding polypeptides with cytokine-like activities, useful
in diagnosis and gene therapy.
Claim 20; Page 3461-3462; 6221pp; English.
The invention relates to polynucleotides (AAK51456-AAK53435) and the
encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
cytokine, cell proliferation or cell differentiation which may induce
production of other cytokines in other cell populations. The
polynucleotides and polypeptides are useful in gene therapy, vaccines or
peptide therapy. The polypeptides have various cytokine-like activities,
e.g. stem cell growth factor activity, haematopoiesis regulating
activity, tissue growth factor activity, immunomodulatory activity and
activin/inhibin activity and may be useful in the diagnosis and/or
treatment of cancer, leukaemia, nervous system disorders, arthritis and
inflammation. Note: Records for SEQ ID NO 2110 (AAKS2581), 2111
(AAKS2582) and 3666 (AAM80020) are omitted as the relevant pages from the
sequence listing were missing at the time of publication
SQ Sequence 166 AA;
Alignment Scores:
Pred. No.: 1,246-66 Length: 166
Score: 699.00 Matches: 134
Percent Similarity: 89.76% Conservative: 15
Best Local Similarity: 80.72% Mismatches: 17
Query Match: 77.58% Indels: 0
DB: 4 Gaps: 0
US-10-649-952A-2 (1-501) x AAM78545 (1-166)
QY 1 ATGCGCTCCGGTGTGGTGTCCTCTCATAGGTGTTCACACGACATGAAGTGC 60
DB 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20
QY 61 CGTAAGTCTTCAAGCCAGGAGGTGAGAACGCCGAAGAGCGGGTGTCTTCGCTGC 120
DB 21 ArgLysSerSerThrGlnGluGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40
QY 121 AGTGAGGACAAGAACAATCATCTCTGGAGGAGGCGCAAGAGATCTGTGGCGCATGTG 180
DB 41 SerAspAspLysArgGlnIleValGluGluAlaLysGlnIleLysAlaValLeuPheCysLeu 100
QY 181 GCGCAGACTGTCAGCATCCCTTACGACATGCTGCTGCAAGATGCTGCCAGATAAGACTGC 240
DB 61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 80
QY 241 CGCTATGCCCTCTATGATGCAACCTATGAGACCAAGAGAGCAAGAGAGGATCTGGTG 300
DB 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
QY 301 TTTATCTTCTGGCCCCCGAGTCTGCGCCCTTAAGACAAATGATTATTCAGCTCC 360
DB 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
QY 361 AAGGACGCCATCAAGAAGAAGCTGACAGGATCAAGCATGAATTCGAAGCAAACCTGCTAC 420
DB 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 140
QY 421 GAGGAGGTCAAGGACCGCTGACCCTGCGAGAGAGTGGGGGCGAGTGGCGGTCTATCTCC 480
DB 141 AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyGlyAsnValValIleSer 160
QY 481 CTGGAGGGCAAGCCTTTTG 498
DB 161 LeuGluGlyLysProLeu 166

RESULT 12

AD75248
ID ADB75248 standard; protein; 166 AA.
XX
AC ADB75248;
XX
DT 04-DEC-2003 (first entry)
XX
DE Prostate cancer marker protein.
XX
KW Prostate; cancer; cytostatic; gene therapy; marker.
XX
OS Homo sapiens.
XX
PN WO2003009814-A2.
XX
PD 06-FEB-2003.
XX
PF 25-JUL-2002; 2002WO-US023913.
XX
PR 25-JUL-2001; 2001US-0307982P.
PR 22-AUG-2001; 2001US-0314356P.
PR 25-SEP-2001; 2001US-0325020P.
PR 12-DEC-2001; 2001US-0341746P.
PR 05-MAR-2002; 2002US-0362158P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
PI Hoersh S, Kamatkar S, Woney AM, Glatk K, Zhao X, Anderson D;
XX
DR WPI; 2003-248033/24.
XX
PT New nucleic acid molecule, useful for diagnosing or treating prostate cancer.
XX
PS Disclosure; SEQ ID NO 72; 99pp; English.
XX
CC The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer. Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 166 AA;

Alignment Scores:
Pred. No.: 1.24e-66 Length: 166
Score: 699.00 Matches: 134
Percent Similarity: 89.76% Conservative: 15
Best Local Similarity: 80.72% Mismatches: 17
Query Match: 77.58% Indels: 0
DB: 7 Gaps: 0

US-10-649-952A-2 (1-501) x ADB75248 (1-166)

Qy 1 ATGGCTCCGGTGGCTGCTCTGCTGCTCATCAAGGTGTTCAACGACATCAAGGTG 60
Db 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20

Qy 61 CGTAAGTCTTCAACGCCCAAGAGAGGTGAAGAGCGCAAGAGCGCGGTCTCTTCGCTG 120
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Qy 121 AGTGAGGACAAGAAACATCATCTGGAGGAGGCAAGAGATCCTGTGGCGCATGTG 180
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Qy 481 CTGAGGGCAAGCCTTTG 498
Db 161 LeuGluGlyLysProLeu 166

RESULT 13
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ID ADJ70104 standard; protein; 166 AA.
XX
AC ADJ70104;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID1910.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.
XX
PS Claim 1; SEQ ID NO 1910; 180pp; English.

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RESULT 14	
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DT 15-APR-2004 (first entry)	
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Db 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTyrGlnValAsnGlyLeu 140
Qy 421 GAGGAGGTCAAGGACCGCTGACACCTGCGCAGAGAGCTGGGGGCGAGTCCGCTCATCTCC 480
Db 141 AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyAsnValValSer 160
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Db 161 LeuGluGlyLysProLeu 166
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ID AAU18546 standard; protein; 205 AA.
XX
AC AAU18546;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human cytoskeletal element-related polypeptide #39.
XX
KW Cytoskeletal element-related protein; human; mouse; rabbit; goat; horse;
KW cat; dog; chicken; sheep; immunosuppressive; antarthritic; vasotropic;
KW antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective;
KW cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;
KW ophthalmological; vulnary; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; breast; liver; cardiovascular disorder;
KW cerebrovascular disorder; nervous system disorder; bacterial infection;
KW fungal infection; viral infection; ocular disorder; endocrine disorder;
KW gastrointestinal disorder; renal disorder; respiratory disorder;
KW wound healing; skin aging; organ transplantation; food preservative;
KW tissue regeneration; anti-infertility; food additive.
XX
OS Homo sapiens.
XX
FN WO200155168-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001331.
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 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-476182/51.
 N-PSDB; AAS29808.

Novel isolated human cytoskeletal element-related polypeptide useful for diagnosis/treatment of neoplastic disorders, disorders associated with neural transmission, chromosomal abnormalities, autoimmune disorders.

Claim 11; SEQ ID NO 93; 505pp; English.

Sequences AAU18508-AAU18551 represent the cytoskeletal element-related polypeptides of the invention. Cytoskeletal polypeptides and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by determining the presence or absence of a mutation in a cytoskeletal polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral ischaemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate

CC tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities.
 CC Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences

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 QY 61 CGTAAGTCTTCAACGCCAGAGGAGGTGAAGAGCGCAAGAGCGCGGTCTTCTTCGCTG 120
 DB ArgLysSerSerThrGlnGluLysLysLysLysLysLysLysLysLysLysLysLys 79
 QY 121 AGTGAGGACAAGAACATCATCTCTGGAGAGGGCAAGAGAGATCTGTGGCGGATGTG 180
 DB SerAspLysArgGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLys 99
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 QY 241 CGCTATGCCCTCTATGATCAACCTATGAGACCAAGAGAGCAAGAGAGGATCTCGGTG 300
 DB ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 139
 QY 301 TTTATCTTCTGGGCCCCGAGTCTGGCCCCCTTTAAGAGCAAAATGATTTATGCAGCTCC 360
 DB PheLeuPheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 159
 QY 361 AAGGAGCCCATCAAGAGAGCTGACAGGGATCAAGCATGATTTGCAAGCAAACTGCTAC 420
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 QY 421 GAGGAGGTCAAGGACCGCTGCACCCCTGGCAGAGAGCTGGGGGCGAGTCCGTCATCTCC 480
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 QY 481 CTGGAGGGCAAGCCTTTG 498
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GenCore version 5.1.6
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Searched: 283416 seqs, 96216763 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	842	93.5	166	2 S49101	cofilin - rat
3	841	93.3	166	1 A29240	cofilin - pig
4	839	93.1	166	1 S12584	cofilin - mouse
5	702	77.9	166	2 A53812	cofilin, muscle -
6	701	77.8	166	1 B35703	cofilin - chicken
7	620.5	68.9	165	1 A35702	desrin - chicken
8	606.5	67.3	165	1 A35179	desrin - pig
9	606.5	67.3	165	1 A54184	desrin [validated
10	598.5	66.4	164	2 JE0223	desrin - rat
11	267.5	29.7	143	1 A4397	cofilin - yeast (S
12	254	28.2	137	2 T43245	probable actin-dep
13	227	25.2	139	2 T02914	actin-depolymerizi
14	213	23.6	140	2 A86149	actin-depolymerizi

15	208	23.1	132	2	G84717	actin depolymerizi
16	208	23.1	139	2	T02883	actin-depolymerizi
17	205.5	22.8	142	2	S71361	actin-binding prot
18	201.5	22.4	148	2	A57569	twinstar protein -
19	200.5	22.3	133	2	T01232	actin-depolymerizi
20	200.5	22.3	139	2	S30935	actin-depolymerizi
21	195.5	21.7	130	2	T47540	actin-depolymerizi
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23	192.5	21.4	139	2	T02882	actin-depolymerizi
24	191	21.2	126	2	S30934	actin-depolymerizi
25	190.5	21.1	130	2	T05788	actin-depolymerizi
26	187	20.8	132	2	B84543	actin depolymerizi
27	185.5	20.6	135	2	T49327	cofilin related pr
28	176.5	19.6	58	2	A56448	desrin-like prote
29	158.5	17.6	133	2	T47539	actin depolymerisi
30	157.5	17.5	49	2	B56448	cofilin-like prote
31	150.5	16.7	165	2	S41728	actin depolymerizi
32	149.5	16.6	293	2	T33952	actin depolymerizi
33	130	14.4	152	2	S41727	unc-60 protein - C
34	120	13.3	350	2	A59222	tyrosine kinase A6
35	104	11.5	349	2	T46362	probable tyrosine
36	102.5	11.4	221	2	C34768	ORF2 protein - Orf
37	101	11.2	200	2	S54834	HP8 peptide - huma
C 38	101	10.9	1958	2	B40505	hypothetical prote
C 39	98.5	10.9	358	2	T13017	hypothetical prote
C 40	98	10.9	328	2	T40910	probable tyrosine
C 41	97	10.5	1446	1	A45344	immediate-early pr
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C 43	96	10.7	141	1	JDB08	glia maturation fa
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C 45	95	10.2	373	2	B75276	DNA-binding respon

ALIGNMENTS

RESULT 1

S12632

cofilin - human

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C;Accession: S12632

R;Gawara, K.; Tashima, M.; Yumoto, Y.; Okuda, T.; Sawada, H.; Okuma, M.; Maruyama, Y.

Nucleic Acids Res. 18, 7169, 1990

A;Title: Coding sequence of human placenta Cofilin cDNA.

A;Reference number: S12632; MUID:91088330; PMID:2263493

A;Accession: S12632

A;Molecule type: mRNA

A;Residues: 1-166 <OGA>

A;Cross-references: UNIPROT:P23528; EMBL:D00682; NID:g219544; PIDN:BAA00589.1; PID:g21954

C;Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a p

C;Genetics:

A;Gene: GDB:CFL1; CFL

A;Cross-references: GDB:126798; OMIM:601442

A;Map position: l1q3-11q3

C;Superfamily: cofilin

C;Keywords: actin binding; phosphoprotein

F;26-36/Region: nuclear location signal

F;104-134/Region: actin binding #status predicted

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Db 141 GluGluVallylsAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer 160
Qy 481 CTGAGGCGCAAGCCTTTG 498
Db 161 LeuGluGlyLysProLeu 166
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cofilin - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Jan-1995 #sequence revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S49101; A58860; J0222
R:Shirasawa, T.; Takahashi, H.; Sakamoto, K.; Kawashima, A.; Akashi, T.
submitted to the EMBL Data Library, October 1991
A:Description: Nucleotide sequence of rat cofilin cDNA.
A:Reference number: S49101
A:Accession: S49101
A:Molecule type: mRNA
A:Residues: 1-166 <SH2>
A:Cross-references: UNIPROT:P45592; EMBL:X62908; NID:G509200; PIDN:CAA44694.1; PID:G50920
R:Shirasawa, T.
submitted to DDBJ, October 1991
A:Reference number: A58860
A:Accession: A58860
A:Molecule type: mRNA
A:Residues: 1-166 <SH2>
A:Cross-references: EMBL:X62908; NID:G509200; PIDN:CAA44694.1; PID:G509201
A:Experimental source: embryo brain
R:Kanamori, T.; Suzuki, M.M.; Titani, K.
submitted to JPIPD, August 1998
A:Description: Complete amino acid sequences and phosphorylation sites, determined by Ed
A:Reference number: J0222
A:Accession: J0222
A:Molecule type: protein
A:Residues: 2-166 <KAN>
C:Superfamily: cofilin
C:Keywords: acetylated amino end; phosphoprotein
F:2-166/Product: cofilin #status experimental <MAT>
F:19-34/Region: nuclear location signal
F:104-115/Region: actin binding #status predicted
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F:3/Binding site: phosphate (Ser) (covalent) #status experimental
Alignment Scores:
Pred. No.: 2,99e-66 Length: 166
Score: 842.00 Matches: 165
Percent Similarity: 99.40% Conservative: 0
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Best Local Similarity: 99.40% Mismatches: 1
Query Match: 93.45% Indels: 0
DB: 2 Gaps: 0
US-10-649-952A-2 (1-501) x S49101 (1-166)
Qy 1 ATGGCCTCCGGTGGGCTGCTCTGATGGTGTCTCATCAAGGTGTTCAACGACATGAAGGTG 60
Db 1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAenaspMetLysVal 20
Qy 61 CGTAAGTCTTCAACGCCAGAGGAGGTGAAGAAGCGCAAGAGCGGCTCTTCTGCTG 120
Db 21 ArglysserSerThrProGluGluVallylsysarglylsAlaValLeuPheCysLeu 40
Qy 121 AGTGAGGCAAGAAGAATCATCTCTGAGGAGGCGCAAGGAGATCCTGGTGGCGATGTG 180
Db 41 SerGluaspLysLysAenilleleuGluGluGlyLysGluilleLeuValGlyAspVal 60
Qy 181 GCCAGACTGTGAGGATCCCTAGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
Db 61 GlyGlnThrValaspAspProTyrThrPheValLysMetLeuProaspLysAspCys 80
Qy 241 CGCTATGCCCTCTATGATGCAACCTATGAGACCAAGAGAGCAAGAAGGAGATCTGGTG 300
Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluaspLeuVal 100
Qy 301 TTTATCTTCTGGGCCCCGAGTCTGCGCCCCCTTAAGAGCAAAATGATTTATGCGAGCTCC 360
Db 101 PheilePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
Qy 361 AAGACGCCATCAAGAGAAGCTGACAGGATCAAGCATGAATTCGAAGCAACTGCTAC 420
Db 121 LysaspAlaIleLysLysLysLeuThrGlyLysHisGluLeuGlnAlaAsnCysTyr 140
Qy 421 GAGGAGGTCAAGGACCGCTGCACCTGCGCAGAGAGCTGGGGGCGAGTGGCGGTTCATCTCC 480
Db 141 GluGluVallylsAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer 160
Qy 481 CTGAGGCGCAAGCCTTTG 498
Db 161 LeuGluGlyLysProLeu 166
RESULT 3
A29240
cofilin - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 28-Aug-1989 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A29240
R:Matsuzaki, F.; Matsumoto, S.; Yahara, I.; Yonezawa, N.; Nishida, E.; Sakai, H.
J. Biol. Chem. 263, 11564-11568, 1988
A:Title: Cloning and characterization of porcine brain cofilin cDNA. Cofilin contains th
A:Reference number: A29240; MUID:88298817; PMID:3403546
A:Accession: A29240
A:Molecule type: mRNA
A:Residues: 1-166 <MAT>
A:Cross-references: UNIPROT:P10668; GB:M20866; NID:G164424; PIDN:AAA31020.1; PID:G164425
C:Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a p
C:Keywords: actin binding; phosphoprotein
F:26-36/Region: nuclear location signal
F:104-134/Region: actin binding #status predicted
Alignment Scores:
Pred. No.: 3.67e-66 Length: 166
Score: 841.00 Matches: 165
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 1
Query Match: 93.34% Indels: 0
DB: 1 Gaps: 0
US-10-649-952A-2 (1-501) x A29240 (1-166)
Qy 1 ATGGCCTCCGGTGGGCTGCTCTGATGGTGTCTCATCAAGGTGTTCAACGACATGAAGGTG 60
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Db      1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20
QY      61 CGTAAGTCTTCAAGCCGAGAGGAGGTGAAGAAGCGCAAGAAGCGGTGCTCTTCTGCGCTG 120
Db      21 ArgLysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
QY      121 AGTGAGACAAAGAAGAACATCATCTCGAGAGGCGCAAGAGATCTCTGGTGGCGATGTG 180
Db      41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
QY      181 GGCACAGCTCTGACGATCCCTACGCCACCTTGTCAAGATGCTGAGAGGAGGATCTGGTG 240
Db      61 GlyGlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCys 80
QY      241 CGTATGCTCTCTATGATCAACCTATGAGACCAAGAGGAGGAGGAGGATCTGGTG 300
Db      81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysGluAspLeuVal 100
QY      301 TTTATCTTCTGGCCCCCGAGCTGCGCCCTTAAAGAGCAAAATGATTTATGCGAGCTCC 360
Db      101 PheIlePheTrpAlaProGluCysAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
QY      361 AAGGACCCATCAAGAAGAGCTGACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
Db      121 LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyr 140
QY      421 GAGGAGGTCAAGGACCGCTGCACCTGGCAGAGAGCTGGGGGCGAGTGGCGTCATCTCC 480
Db      141 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlySerAlaValIleSer 160
QY      481 CTGAGGGCAAGCCTTTG 498
Db      161 LeuGluGlyLysProLeu 166

RESULT 4
S12584
Cofillin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: S12584; J00201
R;Moriyama, K.; Matsumoto, S.; Nishida, E.; Sakai, H.; Yahara, I.
Nucleic Acids Res. 18, 3053, 1990
A;Title: Nucleotide sequence of mouse cofillin cDNA.
A;Reference number: S12584; MUID:90272419; PMID:2349104
A;Accession: S12584
A;Molecule type: mRNA
A;Residues: 1-166 <MOR>
A;Cross-references: UNIPROT:P18760; EMBL:D00472; NID:g220383; PIDN:BAA00364.1; PID:g2203
C;Comment: Cofillin reversibly regulates actin polymerization and depolymerization in a p
C;Superfamily: cofillin
F;28-36/Region: actin binding; phosphoprotein
F;104-134/Region: actin binding #status predicted

Alignment Scores:
Pred. No.: 5 5e-66 Length: 166
Score: 839.00 Matches: 164
Percent Similarity: 99.40% Conservative: 1
Best Local Similarity: 98.80% Mismatches: 0
Query Match: 93.12% Indels: 0
DB: 1 Gaps: 0

US-10-649-952A-2 (1-501) x S12584 (1-166)

QY      1 ATGGCTCCGGTGGGTGCTCTGATGTGTCATCAAGGTGTTCAACGACATGAAGGTG 60
Db      1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20
QY      61 CGTAAGTCTTCAAGCCGAGAGGAGGTGAAGAAGCGCAAGAAGCGGTGCTCTTCTGCGCTG 120
Db      21 ArgLysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
QY      121 AGTGAGACAAAGAAGAACATCATCTCGAGAGGCGCAAGAGATCTCTGGTGGCGATGTG 180
Db      41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
QY      181 GGCACAGCTCTGACGATCCCTACGCCACCTTGTCAAGATGCTGAGAGGAGGATCTGGTG 240
Db      61 GlyGlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCys 80
QY      241 CGTATGCTCTCTATGATCAACCTATGAGACCAAGAGGAGGAGGAGGATCTGGTG 300

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QY      121 AGTGAGACAAAGAAGAACATCATCTCGAGAGGCGCAAGAGATCTCTGGTGGCGATGTG 180
Db      41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
QY      181 GGCACAGCTCTGACGATCCCTACGCCACCTTGTCAAGATGCTGAGAGGAGGATCTGGTG 240
Db      61 GlyGlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCys 80
QY      241 CGTATGCTCTCTATGATCAACCTATGAGACCAAGAGGAGGAGGAGGATCTGGTG 300
Db      81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysGluAspLeuVal 100
QY      301 TTTATCTTCTGGCCCCCGAGCTGCGCCCTTAAAGAGCAAAATGATTTATGCGAGCTCC 360
Db      101 PheIlePheTrpAlaProGluAsnAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
QY      361 AAGGACCCATCAAGAAGAGCTGACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
Db      121 LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyr 140
QY      421 GAGGAGGTCAAGGACCGCTGCACCTGGCAGAGAGCTGGGGGCGAGTGGCGTCATCTCC 480
Db      141 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlySerAlaValIleSer 160
QY      481 CTGAGGGCAAGCCTTTG 498
Db      161 LeuGluGlyLysProLeu 166

RESULT 5
A53812
Cofillin, muscle - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: A53812
R;Ono, S.; Minami, N.; Abe, H.; Obinata, T.
J. Biol. Chem. 269, 15280-15286, 1994
A;Title: Characterization of a novel cofillin isoform that is predominantly expressed in
A;Reference number: A53812; MUID:94253093; PMID:8195165
A;Accession: A53812
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-166 <ONO>
A;Cross-references: UNIPROT:P45591; GB:I29468; NID:g498016; PIDN:AAA37433.1; PID:g498017
C;Superfamily: cofillin
C;Keywords: actin binding; muscle

Alignment Scores:
Pred. No.: 6 57e-54 Length: 166
Score: 702.00 Matches: 135
Percent Similarity: 89.76% Conservative: 14
Best Local Similarity: 81.33% Mismatches: 17
Query Match: 77.91% Indels: 0
DB: 2 Gaps: 0

US-10-649-952A-2 (1-501) x A53812 (1-166)

QY      1 ATGGCTCCGGTGGGTGCTCTGATGTGTCATCAAGGTGTTCAACGACATGAAGGTG 60
Db      1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20
QY      61 CGTAAGTCTTCAAGCCGAGAGGAGGTGAAGAAGCGCAAGAAGCGGTGCTCTTCTGCGCTG 120
Db      21 ArgLysSerSerThrGlnGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40
QY      121 AGTGAGACAAAGAAGAACATCATCTCGAGAGGCGCAAGAGATCTCTGGTGGCGATGTG 180
Db      41 SerAspAspLysArgGlnIleIleValGluGluAlaLysGlnIleLeuValGlyAspIle 60
QY      181 GGCACAGCTCTGACGATCCCTACGCCACCTTGTCAAGATGCTGCCAGATGAAGGACTGC 240
Db      61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 80
QY      241 CGTATGCTCTCTATGATCAACCTATGAGACCAAGGAGGAGGAGGATCTGGTG 300

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Db 81 ArgIyAlaLeuTyAspAlaThrTyGluThrLysGluSerLysLysGluAspLeuVal 100
Qy 301 TTTATCTCTGGGCCCCGAGCTGCGCCCTTAAGAGCAAAATGATTATGCCAGCTCC 360
Db 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyAlaSerSer 120
Qy 361 AAGGACGCCATCAAGAAGAGCTCACAGGGATCAAGCATGAATTCGAAGCAAACTGCTAC 420
Db 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 140
Qy 421 GAGGAGTCAAGACCGCTGCACCTGCAGAGAGCTGGGGCGAGTGGCGGTCAATCTCC 480
Db 141 AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyGlySerValValValSer 160
Qy 481 CTGAGGGCAAGCCTTTG 498
Db 161 LeuGluGlyLysProLeu 166
RESULT 6
B35703
cofilin - chicken
C:Species: Gallus gallus (chicken)
C>Date: 12-Oct-1990 #sequence_revision 27-Jun-1994 #text_change 22-Jun-1999
C:Accession: B35703
R:Abbe, H.; Endo, T.; Yamamoto, K.; Obinata, T.
Biochemistry 29, 7420-7425, 1990
A:Title: Sequence of cDNAs encoding actin depolymerizing factor and cofilin of embryonic
A:Reference number: A35703; MUID:91027755; PMID:1699599
A:Accession: B35703
A:Molecule type: mRNA
A:Residues: 1-166 <ABE>
A:Cross-references: GB:M55659; NID:g211569; PIDN:AAA62732.1; PID:g211570; GB:J02915
C:Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a p
C:Superfamily: cofilin
C:Keywords: actin binding; phosphoprotein
F:26-36/Region: nuclear location signal
F:104-134/Region: actin binding #status predicted
Alignment Scores:
Pred. No.: 8.04e-54 Length: 166
Score: 701.00 Matches: 135
Percent Similarity: 88.55% Conservative: 12
Best Local Similarity: 81.33% Mismatches: 19
Query Match: 77.80% Indels: 0
DB: 1 Gaps: 0
US-10-649-952A-2 (1-501) x B35703 (1-166)
Qy 1 ATGCGCTCCGGTGGCTGCTCTGATGGTGTCTCAAGGTGTTCACGACATCAAGGTG 60
Db 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20
Qy 61 CGTAAGTCTTCAACGCAGAGAGGTGAAGAAGCGCAAGAGCGGTGCTCTTCGCTG 120
Db 21 ArgLysSerSerThrProGluGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40
Qy 121 AGTGAGGACAAAGAACAATCATCTCTGGAGGAGGCGCAAGGAGATCCTGGTGGCGATGTG 180
Db 41 SerAspAspLysLysGlnIleValGluGluAlaThrArgIleLeuValGlyAspIle 60
Qy 181 GGCAGACTGTGAGCATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
Db 61 GlyAspThrValGluAspProTyThrAlaPheValLysLeuLeuProLeuAsnAspCys 80
Qy 241 CGCTATGCGCTCTATGATGCAACCTATGAGACCAAGGAGGACCAAGGAGGATCTGGTG 300
Db 81 ArgIyAlaLeuTyAspAlaThrTyGluThrLysGluSerLysLysGluAspLeuVal 100
Qy 301 TTTATCTCTGGGCCCCGAGCTGCGCCCTTAAGAGCAAAATGATTATGCCAGCTCC 360
Db 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyAlaSerSer 120
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Qy 361 AAGGACGCCATCAAGAAGAGCTCACAGGATCAAGCATGAATTCGAAGCAAACTGCTAC 420
Db 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 140
Qy 421 GAGGAGTCAAGACCGCTGCACCTGCAGAGAGCTGGGGCGAGTGGCGGTCAATCTCC 480
Db 141 AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyGlyAsnValValValSer 160
Qy 481 CTGAGGGCAAGCCTTTG 498
Db 161 LeuGluGlyLysProLeu 166
RESULT 7
A35702
desrin - chicken
N:Alternate names: actin-depolymerizing factor
C:Species: Gallus gallus (chicken)
C>Date: 12-Oct-1990 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C:Accession: A35702; A35703; A40672
R:Adams, M.E.; Minamide, L.S.; Duester, G.; Bamburg, J.R.
Biochemistry 29, 7414-7420, 1990
A:Title: Nucleotide sequence and expression of a cDNA encoding chick brain actin depolym
A:Reference number: A35702; MUID:91027754; PMID:2223773
A:Accession: A35702
A:Molecule type: mRNA
A:Residues: 1-165 <ADA>
A:Cross-references: UNIPROT:P18359; GB:J02912; NID:g211096; PIDN:AAA48575.1; PID:g211097
A:Experimental source: brain
A:Note: part of this sequence was confirmed by peptide sequencing
R:Abbe, H.; Endo, T.; Yamamoto, K.; Obinata, T.
Biochemistry 29, 7420-7425, 1990
A:Title: Sequence of cDNAs encoding actin depolymerizing factor and cofilin of embryonic
A:Reference number: A35703; MUID:91027755; PMID:1699599
A:Accession: A35703
A:Molecule type: mRNA
A:Residues: 1-165 <ABE>
A:Cross-references: GB:M55660; GB:J02915; NID:g211092; PIDN:AAA48573.1; PID:g211093
A:Experimental source: muscle
A:Note: part of this sequence was confirmed by peptide sequencing
R:Morgan, T.E.; Lockerbie, R.O.; Minamide, L.S.; Browning, M.D.; Bamburg, J.R.
J. Cell Biol. 122, 623-633, 1993
A:Title: Isolation and characterization of a regulated form of actin depolymerizing fact
A:Reference number: A40672; MUID:93328764; PMID:7687605
A:Accession: A40672
A:Molecule type: protein
A:Residues: 20-30 <MOR>
R:Agnew, B.J.; Minamide, L.S.; Bamburg, J.R.
J. Biol. Chem. 270, 17582-17587, 1995
A:Title: Reactivation of phosphorylated actin depolymerizing factor and identification c
A:Reference number: A38989; MUID:9340558; PMID:7615564
A:Contents: annotation; acetylated amino end; phosphorylation site
C:Comment: Desrin is an actin-binding protein that is capable of rapidly depolymerizing
C:Superfamily: cofilin
C:Keywords: acetylated amino end; actin binding; phosphoprotein
F:2-165/Product: desrin #status predicted <MA>
F:26-36/Region: nuclear location signal
F:104-134/Region: actin binding #status predicted
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F:3/Binding site: phosphate (Ser) (covalent) #status experimental
Alignment Scores:
Pred. No.: 1e-46 Length: 165
Score: 620.50 Matches: 122
Percent Similarity: 84.34% Conservative: 18
Best Local Similarity: 73.49% Mismatches: 25
Query Match: 68.87% Indels: 1
DB: 1 Gaps: 1
US-10-649-952A-2 (1-501) x A35702 (1-165)
Qy 1 ATGCGCTCCGGTGGCTGCTCTGATGGTGTCTCATCAAGGTGTTCACGACATCAAGGTG 60
```

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Db 1 MetAlaSerGlyValGlnValAlaAspGluValCysArgIlePheTyrAspMetLysVal 20
|||||
QY 61 CGTAAGTCTTCAAGCCGAGAGGAGGTCAAGAACGCGCAAGAGCGGTCTCTTCTGCCTG 120
|||||
Db 21 ArgLysCysSerThrProGluGluValLysLysArgLysLysAlaValIlePheCysLeu 40
|||||
QY 121 AGTGAGGACAAAGAACATCATCTCTGGAGAGGCGCAAGAGATCCTGGTGGCGGATGTG 180
|||||
Db 41 SerProAspLysLysCysIleIleValGluGluGlyLysGluIleLeuValGlyAspVal 60
|||||
QY 181 GGCACAGCTCTCAGCATCCCTACGCCCTTGTCAAGATGCTGCCAGATAGGACTGC 240
|||||
Db 61 GlyValThrValThrAspProPheLysHisPheValGlyMetLeuProGluLysAspCys 80
|||||
QY 241 CGCTATGCCCTCTATGATGCAACCTATGAGACCAAGAGAGGAGGAGGATCTGGTG 300
|||||
Db 81 ArgTyrAlaLeuTyrAspAlaSerPheGluThrLysGluSerLysLysGluGluLeuMet 100
|||||
QY 301 TTTATCTTCTGGCCCCCGAGTCTGCGCCCTTAAAGAGCAAAATGATTTATGCGAGCTCC 360
|||||
Db 101 PhePheLeuTrpAlaProGluGlnAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
|||||
QY 361 AAGGAGCCATCAAGAGAGCTGACAGGATCAAGCATCAATTCGAAGCAAACTGCTAC 420
|||||
Db 121 LysAspAlaIleLysLysPheGlnGlyIleLysHisGluCysGlnAlaAsnGlyPro 140
|||||
QY 421 GAGGAGGTCAAGACCGCTGCACCTGGCAGAGAGCTGGGGGCGAGTGGCGTCATCTCC 480
|||||
Db 141 GluAspLeuAsnArgAlaCys---IleAlaGluLysLeuGlySerLeuValAlaAla 159
|||||
QY 481 CTGAGGGCAAGCCTTTG 498
|||||
Db 160 PheGluGlySerProVal 165
|||||

RESULT 8
A35179
destrin - pig
N;Alternate names: actin-depolymerizing factor
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 03-Aug-1990 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C;Accession: A35179
R;Moriyama, K.; Nishida, E.; Yonezawa, N.; Sakai, H.; Matsumoto, S.; Iida, K.; Yahara, I.
J. Biol. Chem. 265, 5768-5773, 1990
A;Title: Destrin, a mammalian actin-depolymerizing protein, is closely related to cofilin
A;Reference number: A35179; MUID:90202824; PMID:2156828
A;Accession: A35179
A;Molecule type: mRNA
A;Residues: 1-165 <MOR>
A;Cross-references: UNIPROT:P60982; GB:D90053; GB:J05290; NID:G217681; PIDN:BAAL14105.1;
A;Experimental source: brain
C;Comment: Destrin is an actin-binding protein that is capable of rapidly depolymerizing
C;Superfamily: cofilin
C;Keywords: acetylated amino end; actin binding; phosphoprotein
F;2-165/Product: destrin #status predicted <MAT>
F;26-36/Region: nuclear location signal
F;104-134/Region: actin binding #status predicted
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
F;3/Binding site: phosphate (Ser) (covalent) #status predicted

Alignment Scores:
Pred. No.: 1.72e-45 Length: 165
Score: 606.50 Matches: 118
Percent Similarity: 83.73% Conservative: 21
Best Local Similarity: 71.08% Mismatches: 26
Query Match: 67.31% Indels: 1
DB: 1 Gaps: 1

US-10-649-952A-2 (1-501) x A35179 (1-165)
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QY 61 CGTAAGTCTTCAAGCCGAGAGGAGGTCAAGAACGCGCAAGAGCGGTCTCTTCTGCCTG 120
|||||
Db 21 ArgLysCysSerThrProGluGluIleLysLysArgLysLysAlaValIlePheCysLeu 40
|||||
QY 121 AGTGAGGACAAAGAACATCATCTCTGGAGAGGCGCAAGAGATCCTGGTGGCGGATGTG 180
|||||
Db 41 SerAlaAspLysLysCysIleIleValGluGluGlyLysGluIleLeuValGlyAspVal 60
|||||
QY 181 GGCACAGCTCTCAGCATCCCTACGCCCTTGTCAAGATGCTGCCAGATAGGACTGC 240
|||||
Db 61 GlyValThrIleThrAspProPheLysHisPheValGlyMetLeuProGluLysAspCys 80
|||||
QY 241 CGCTATGCCCTCTATGATGCAACCTATGAGACCAAGAGAGGAGGAGGATCTGGTG 300
|||||
Db 81 ArgTyrAlaLeuTyrAspAlaSerPheGluThrLysGluSerLysLysGluGluLeuMet 100
|||||
QY 301 TTTATCTTCTGGCCCCCGAGTCTGCGCCCTTAAAGAGCAAAATGATTTATGCGAGCTCC 360
|||||
Db 101 PhePheLeuTrpAlaProGluLeuAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
|||||
QY 361 AAGGAGCCATCAAGAGAGCTGACAGGATCAAGCATCAATTCGAAGCAAACTGCTAC 420
|||||
Db 121 LysAspAlaIleLysLysPheGlnGlyIleLysHisGluCysGlnAlaAsnGlyPro 140
|||||
QY 421 GAGGAGGTCAAGACCGCTGCACCTGGCAGAGAGCTGGGGGCGAGTGGCGTCATCTCC 480
|||||
Db 141 GluAspLeuAsnArgAlaCys---IleAlaGluLysLeuGlySerLeuIleValAla 159
|||||
QY 481 CTGAGGGCAAGCCTTTG 498
|||||
Db 160 PheGluGlyCysProVal 165
|||||

RESULT 9
A54184
destrin [validated] - human
N;Alternate names: actin-depolymerizing factor (ADF)
C;Species: Homo sapiens (man)
C;Date: 13-Sep-1994 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: A54184
R;Hawkins, M.; Pope, B.; MacIver, S.K.; Weeds, A.G.
Biochemistry 32, 9985-9993, 1993
A;Title: Human actin depolymerizing factor mediates a pH-sensitive destruction of actin
A;Reference number: A54184; MUID:94002009; PMID:8399167
A;Accession: A54184
A;Molecule type: mRNA
A;Residues: 1-165 <HAW>
A;Cross-references: UNIPROT:P60981; GB:S65738; NID:G415586; PIDN:AAB28361.1; PID:G415587
A;Experimental source: fetal brain
A;Note: sequence extracted from NCBI backbone (NCBIN:137963, NCBIIP:137964)
R;Hatanaka, H.; Moriyama, K.; Ogura, K.; Ichikawa, S.; Yahara, I.; Inagaki, F.
submitted to the Brookhaven Protein Data Bank, May 1997
A;Reference number: A67992; PDB:IAK6
A;Contents: annotation; conformation by (1)H-, (13)C-, and (15)N-NMR, residues 'TMITPSSG
R;Hatanaka, H.; Ogura, K.; Moriyama, K.; Ichikawa, S.; Yahara, I.; Inagaki, F.
Cell 85, 1047-1055, 1996
A;Title: Tertiary structure of destrin and structural similarity between two actin-regula
A;Reference number: A38990; MUID:96270507; PMID:8674111
A;Contents: annotation; NMR
C;Comment: The unphosphorylated form of destrin is capable of rapidly depolymerizing F-act
C;Genetics:
A;Gene: GDB:ACTDP
A;Cross-references: GDB:249179
C;Superfamily: cofilin
C;Keywords: acetylated amino end; actin binding; phosphoprotein
F;2-165/Product: destrin #status predicted <MAT>
F;26-36/Region: nuclear location signal
F;104-134/Region: actin binding #status predicted
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
F;3/Binding site: phosphate (Ser) (covalent) #status predicted

Alignment Scores:
Pred. No.: 1.72e-45 Length: 165
```

Score: 606.50 Matches: 118
Percent Similarity: 83.73% Conservative: 21
Best Local Similarity: 71.08% Mismatches: 26
Query Match: 67.31% Indels: 1
DB: 1 Gaps: 1

US-10-649-952A-2 (1-501) x A54184 (1-165)

QY 1 ATGGCCCTCGGTGGTCTCTGATGGTGTCTCATCAAGGTGTTCAACGACATGAAGGTG 60
DB 1 MetAlaSerGlyValGlnValAlaAspGluValCysArgIlePheTyrAspMetLysVal 20
QY 61 CGTAAGTCTTCAACGCCAGGAGGTGAAGAGCGCAAGAGCGGCTCTTCTGCGCTG 120
DB 21 ArgLysCysSerThrProGluGluIleLysLysArgLysLysAlaValIlePheCysLeu 40
QY 121 AGTGAGCAAGAAGACATCATCTCTGAGGAGGCGCAAGAGATCTCTGGGCGATGTG 180
DB 41 SerAlaAspLysLysCysIleValGluGluGlyLysGluIleLeuValGlyAspVal 60
QY 181 GGCCAGACTGTCGACGATCCCTACGCCACCTTCTCAAGATGCTGCCAGATAAGACTGC 240
DB 61 GlyValThrIleThrAspProPheLysHisPheValGlyMetLeuProGluLysAspCys 80
QY 241 CGCTATGCTCTATGATCAACCTATGACACCAAGAGAGAGCAAGAGGATCTGGTG 300
DB 81 ArgTyrAlaLeuTyrAspAlaSerPheGluThrLysGluSerArgLysGluLeuMet 100
QY 301 TTTATCTTCTGGGCCCGGAGTCTGCGCCCTTAAGAGCAAAATGATTTATGCCAGTCC 360
DB 101 PhePheLeuTyrAlaProGluLeuAlaProLeuLysSerLysMetIleTyrAlaSer 120
QY 361 AAGCAGCCATCAAGAGAGCTGACAGGGATCAAGCATGAATGCAAGCAAACTGCTAC 420
DB 121 LysAspAlaIleLysLysPheGlnGlyIleLysHisGluCysGlnAlaAsnGlyPro 140
QY 421 GAGGAGTCAAGGACCGCTGACCGCTGCGCAGAGAGCTGGGGGCGAGTGGGTCTATCC 480
DB 141 GluAspLeuAsnArgAlaCys--IleAlaGluLysLeuGlySerLeuIleValAla 159
QY 481 CTGAGGCAAGCCTTTG 498
DB 160 PheGluGlyCysProVal 165

RESULT 10

destrin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C:Accession: JE0223
R:Kanamori, T.; Suzuki, M.M.; Titani, K.
submitted to JIPID, August 1998
A:Description: Complete amino acid sequences and phosphorylation sites, determined by Ed
A:Reference number: JE0222
A:Accession: JE0223
A:Molecule type: protein
A:Residues: 1-164 <KAN>
A:Cross-references: UNIPROT:Q7M0E3
C:Superfamily: coflin
C:Keywords: acetylated amino end; phosphoprotein
F:18-33/Region: nuclear location signal
F:103-114/Region: actin binding #status predicted
F:1/Modified site: acetylated amino end (Ala) #status experimental
F:2/Binding site: phosphate (Ser) (covalent) #status experimental

Alignment Scores:
Pred. No.: 8.72e-45 Length: 164
Score: 598.50 Matches: 115
Percent Similarity: 84.24% Conservative: 24
Best Local Similarity: 69.70% Mismatches: 25
Query Match: 66.43% Indels: 1
DB: 2 Gaps: 1

US-10-649-952A-2 (1-501) x JE0223 (1-164)

QY 4 GCCTCCGCTGGCTGCTCTGATGGTGTCTCATCAAGGTGTTCAACGACATGAAGGTGCGT 63
DB 1 AlaSerGlyValGlnValAlaAspGluValCysArgIlePheTyrAspMetLysValArg 20
QY 64 AAGTCTTCAACGCCAGGAGGTGAAGAGCGCAAGAGCGGCTCTTCTGCTGAGT 123
DB 21 LysCysSerThrProGluGluIleLysLysArgLysLysAlaValIlePheCysLeuSer 40
QY 124 GAGGACAGAGAACATCATCTCTGAGGAGGCGCAAGAGATCTCTGGGCGATGTGGGC 183
DB 41 AlaAspLysLysCysIleValGluGluGlyLysGluIleLeuValGlyAspValGly 60
QY 184 CAGAGTCTGACCATCTCTACGCCACCTTGTCAAGATGCTGCCAGATAAGACTGCCGC 243
DB 61 ValThrIleThrAspProPheLysHisPheValGlyMetLeuProGluLysAspCysArg 80
QY 244 TATGCCCTCTATGATCAACCTATGACACCAAGAGAGCAAGAGGATCTGGTGTGTTT 303
DB 81 TyrAlaLeuTyrAspAlaSerPheGluThrLysGluSerArgLysGluLeuMetPhe 100
QY 304 ATCTTCTGGGCCCGGAGTCTGCGCCCTTAAGAGCAAAATGATTTATGCCAGCTCCAAG 363
DB 101 PheLeuTyrAlaProGluGlnAlaProLeuLysSerLeuMetIleTyrAlaSerSerLys 120
QY 364 GAGCCATCAAGAGAGCTGACAGGGATCAAGCATGAATGCAAGCAAACTGCTACGAG 423
DB 121 AspAlaIleLysLysLysPheProGlyIleLysHisGluTyrGlnAlaAsnGlyProGlu 140
QY 424 GAGTCAAGGACCGCTGACCCCTGGCAGAGAGCTGGGGGCGAGTGGGTCTATCTCCCTG 483
DB 141 AspLeu--AsnArgThrSerIleAlaGluLysLeuGlySerLeuIleValAlaPhe 159
QY 484 GAGGCAAGCCTTTG 498
DB 160 GluGlySerProVal 164

RESULT 11

A44397
cofilin - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein I0595; protein YLL050c
C:Species: Saccharomyces cerevisiae
C:Date: 31-Dec-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A44397; B44397; JN0529; S64802; S50970; S31309; S36087
R:Moore, A.L.; Jamney, P.A.; Louie, K.A.; Drubin, D.G.
J. Cell Biol. 120, 421-435, 1993
A:Title: Cofilin is an essential component of the yeast cortical cytoskeleton.
A:Reference number: A44397; MUID:93132073; PMID:8421056
A:Accession: A44397
A:Molecule type: DNA
A:Residues: 1-143 <MOO>
A:Cross-references: UNIPROT:Q03048; EMBL:Z14971; NID:93563; PIDN:CAA78694.1; PID:93564
A:Note: sequence extracted from NCBI backbone (NCBIN:122683, NCBI:122684)
A:Accession: B44397
A:Molecule type: protein
A:Residues: 43-56;83-96,'X',98,106-129,'DS',132-141 <MO2>
A:Note: sequence extracted from NCBI backbone
R:Iida, K.; Moriyama, K.; Matsumoto, S.; Kawasaki, H.; Nishida, E.; Yahara, I.
Gene 124, 115-120, 1993
A:Title: Isolation of a yeast essential gene, COF1, that encodes a homologue of mammalian
A:Reference number: JN0529; MUID:93178959; PMID:8440472
A:Accession: JN0529
A:Molecule type: DNA
A:Residues: 1-143 <IID>
A:Cross-references: GB:D13230; NID:9287599; PIDN:BAA02514.1; PID:9287600
R:Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64792
A:Accession: S64802
A:Molecule type: DNA
A:Residues: 1-143 <WED>
A:Cross-references: EMBL:Z73155; NID:91360250; PIDN:CAA97502.1; PID:91360251; GSPDB:GN00

A;Molecule type: mRNA
A;Residues: 1-137 <RAW>
A;Cross-references: UNIPROT:P78929; EMBL:D89939; PIDN:BAAL4039.1
R;Connor, R.; Churcher, C.M.; Barrrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z21771
A;Accession: T38120
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-137 <CON>
A;Cross-references: EMBL:Z98600; PIDN:CAB11258.1; GSPDB:GN00066; SPDB:SPAC20G4.066
A;Experimental source: strain 972h-; cosmid C20G4
C;Genetics:
A;Gene: SPAC20G4.06c
A;Map position: 1
A;Introns: 1/3; 37/1
A;Note: adf1
C;Superfamily: cofilin
C;Keywords: actin binding

Alignment Scores:
Pred. No.: 2,02e-14 Length: 137
Score: 254.00 Matches: 53
Percent Similarity: 58.94% Conservatives: 36
Best Local Similarity: 35.10% Mismatches: 42
Query Match: 28.19% Indels: 20
DB: 2 Gaps: 3

US-10-649-952A-2 (1-501) x T43245 (1-137)

QY	7	TCGGTGTGGCTCTCTGATGGTGTCTCAAGGTGTTCAACGACATGAAGTGGCTAAG	66
Db	4	SerGlyValLysValSerProGluCysLeuGluAlaPheGlnGluLeuLysLeuGlyLys	23
QY	67	TCTTCAACCCAGAGAGGTGAAGAGCCCAAGAGCGGTCTCTTCTGCCTGAGTGAG	126
Db	24	Ser-----LeuAArgTyrValValPheLysMetAenAep	34
QY	127	GACAAAGAACAATCATCTCGAGGAGGGCAAGGAGATCTCGTGGCGCATGTGGGCCAG	186
Db	35	ThrLysThrGluIleValValGluLys-----Lys	44
QY	187	ACTGTCGACGATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTCCGCTAT	246
Db	45	SerThrAspLysAspPheAspThrPheLeuGlyAspLeuProGluLysAspCysArgTyr	64
QY	247	GCCTCTATGATGCAACCTATGAGACCAAGGAGAGCAAGAGGAGATCTGCTGTTTATC	306
Db	65	AlaIleTyrAspPheGluPheAsnLeuGlyGluValArgAsnLysIleIlePheIle	84
QY	307	TTCTGGGCCCCGAGTCTCGCCCTTAAGACAAATGATTATGCCAGCTCCAAGGAC	366
Db	85	SerTrpSerProAspValAlaProIleLysSerLysMetValTyrSerSerSerLysAsp	104
QY	367	GCCATCAAGAAGAGCTGACGGGATCAAGCATGAATTGCAAGCAAACTGCTACGAGGAG	426
Db	105	ThrLeuArgAlaPheThrGlyIleGlyThrAspIleGlnAlaThrAspPheSerGlu	124
QY	427	GTCAGGACCGTGCACCTGCACAGAGCTG	459
Db	125	ValAlaTyrGlu---ThrValLeuGluLysVal	134

RESULT 13
T02914
actin-depolymerizing factor 3 - maize
C;Species: Zea mays (maize)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02914
R;Lopez, I.; Anthony, R.G.; Maciver, S.K.; Jiang, C.J.; Khan, S.; Weeds, A.G.; Huss
Proc. Natl. Acad. Sci. U.S.A. 93, 7415-7420, 1996
A;Title: Pollen specific expression of maize genes encoding actin depolymerizing fa
A;Reference number: Z14757; MUID:96293540; PMID:8693008
A;Accession: T02914

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-139 <LOP>

A;Cross-references: UNIPROT:Q41764; EMBL:X97726; NID:g1419369; PIDN:CAA66311.1; PID:g141

A;Experimental source: leaf

C;Genetics:

C;Superfamily: cofillin

C;Keywords: actin binding

Alignment Scores:

Pred. No.:	4.85e-12	Length:	139
Score:	227.00	Matches:	54
Percent Similarity:	54.00%	Conservative:	27
Best Local Similarity:	36.00%	Mismatches:	45
Query Match:	25.19%	Indels:	24
DB:	2	Gaps:	5

US-10-649-952A-2 (1-501) x T02914 (1-139)

Qy	7	TCCGGTGGCTGCTCTCATCAAGGTGTTCAACGACATGAAGTGGTAAG	66
Db	6	SerGlyValAlaValAsnAspGluCysMetLeuLysPheGlyGluLeu	21
Qy	67	TCCTCAACGCCAGAGGAGGTCAAGAAGCCCAAGAGCGGCTCTCTGCTCAGTGAG	126
Db	22	-----GlnSerLysArgLeuHisargPheIleThrPheLysMetAspAsp	36
Qy	127	GACAAGAAGACATCTCTGGAGAGGGCAAGAGATCTCTGGTGGCGATGTGGGCCAG	186
Db	37	LysPheLysGluIleValValAspGln-----ValGlyAspArgAlaThr	51
Qy	187	ACTGTGACGATCCCTACGCCACCTTGTCAAGATGTGCCAGATAGGACTGGCGTAT	246
Db	52	SerTyrAspAsp-----PheThrAsnSerLeuProGluAsnAspCysArgTyr	67
Qy	247	CCCTCTATGATGCAACCTATGACACCAAGAGGAGC---AAGAAGGAGGATCTCGTGT	303
Db	68	AlaIleTyrAspPheAppPheValThrAlaGluAspValGlnLysSerArgIlePheTyr	87
Qy	304	ATCTTCTGGGCCCGGAGTCTGGCCCTTAAGAGCAAAATGATTATGCGAGTCCAAG	363
Db	88	IleLeuTrpSerProSerSerAlaLysValLysSerLysMetLeuTyrAlaSerSerAsn	107
Qy	364	GACCCATCAGACAGACGCTCAGAGGATCAGCATGAATTCAGCAAGCAAC-----	414
Db	108	GlnLysPheLysSerGlyLeuAsnGlyIleGlnValGluLeuGlnAlaThrAspAlaSer	127
Qy	415	-----TGCTACGAGGAGGTCAAGACCGC	438
Db	128	GluLeSerLeuAspGluIleLysAspArg	137

RESULT 14

A86149

actin-depolymerizing factor homolog At1g01750 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: A86149

R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: A86149

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-140 <STO>

A;Cross-references: UNIPROT:Q91Q81; GB:AE005172; NID:98671845; PIDN:AAF78408.1; GSPDB:GN1
C;Genetics:
A;Map position: 1
C;Superfamily: cofillin

Alignment Scores:

Pred. No.:	8.32e-11	Length:	140
Score:	213.00	Matches:	50
Percent Similarity:	57.14%	Conservative:	38
Best Local Similarity:	32.47%	Mismatches:	42
Query Match:	23.64%	Indels:	24
DB:	2	Gaps:	5

US-10-649-952A-2 (1-501) x A86149 (1-140)

Qy	4	GCCTCCGGTGGCTGCTCTCATCAAGGTGTTCAACGACATGAAGTGGT	63
Db	5	AlaSerGlyMetHisValSerAspGluCysLysLeuLysPheLeuGluLeuLys	22
Qy	64	AAGTCTTCAACGCCAGAGGAGGTGAAGAAGCGCAAGAGCGGCTCTCTGCTCAGT	123
Db	23	-----AlaLysArgAsnTyrArgPheIleValPheLysIleAsp	35
Qy	124	GAGGACAGAAGAACAATCATCTCGAGAGGGCAAGAGATCTCTGGTGGCGATGTGGC	183
Db	36	GluLysAlaGlnGlnValMetIleAspLys-----LeuGlyAsnProGlu	50
Qy	184	CAGACTCTCAGCATCTCTAGCCACCTTTGTCAAGATGTGCCAGATAGGACTGGCG	243
Db	51	GluThrTyrGluAsp-----PheThrArgSerIleProGluAspGluCysArg	66
Qy	244	TATGCCCTCTATGATCAACCTATGACACCAAGAGAGC---AAGAAGGAGGATCTCGT	300
Db	67	TyAlaValIleTyrAspTyrAspPheThrProGluAsnCysGlnLysSerLysIlePhe	86
Qy	301	TTTATCTTCTGGCCCCCGAGTCTGGCCCTTAAGAGCAAAATGATTATGCGAGTCC	360
Db	87	PheIleAlaTrpSerProAspThrSerArgValArgSerLysMetLeuTyrAlaSer	106
Qy	361	AAGGACCCATCAAGAAGAAGCTCAGAGGATCAGCATGAATTCAGCAAACTGCTAC	420
Db	107	LysAspArgPheLysArgGluLeuAspGlyIleGlnValGluLeuGlnAlaThrAsp	126
Qy	421	GAGGAG-----GTCAAGGACCGGTGCACCCCTG	447
Db	127	SerGluMetSerLeuAspIleIleLysGlyArgValAsnLeu	140

RESULT 15

G84717

actin depolymerizing factor 6 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C;Accession: G84717

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: G84717

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-132 <STO>

A;Cross-references: GB:AE002093; NID:g4432815; PIDN:AAD20665.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g31200

A;Map position: 2

C;Superfamily: cofillin

Alignment Scores:

Pred. No.:	2.29e-10	Length:	132
Score:	208.00	Matches:	41
Percent Similarity:	63.48%	Conservative:	32

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: May 13, 2005, 09:46:55 ; Search time 137 Seconds
(without alignments)
3745.280 Million cell updates/sec

Title: US-10-649-952A-2
Perfect score: 901
Sequence: 1 atggctccggtgtgctgt.....tggagggaagcctttgtga 501

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p model -DEV=xlp
-Q/cgn2_1/USPTO_spool_p/US10649952/runat_13052005_102649_27313/app_query.fasta_1.647
-DB=Uniprot -Qfmt=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10649952 @CGN 1.1 244 @runat_13052005_102649_27313 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -JONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	841	93.3	165	1	COF1_HUMAN	P23528 homo sapien
2	837	92.9	165	1	COF1_RAT	P45592 rattus norv
3	836	92.8	165	1	COF1_PIG	P10668 sus scrofa
4	836	92.8	165	1	COF1_SHEEP	O6b7m7 ovis aries
5	834	92.6	165	1	COF1_MOUSE	P18760 mus musculus
6	831	92.2	229	2	O9CX22	O9CX22 mus musculus
7	709	78.7	166	1	COF1_CHICK	P21566 gallus gall
8	702	77.9	166	1	COF2_MOUSE	P45591 mus musculus
9	699	77.6	166	1	COF2_HUMAN	O9Y281 homo sapien
10	693	76.9	166	2	O6N2W3	O6N2W3 brachydanio
11	659	73.1	168	2	O6NX11	O6NX11 xenopus tro
12	656	72.8	168	1	COF2_XENLA	P45593 xenopus lae
13	649	72.0	168	1	COF1_XENLA	P45695 xenopus lae
14	625.5	69.4	165	2	O6TH32	O6TH32 brachydanio
15	615.5	68.3	164	1	DEST_CHICK	P18359 gallus gall
16	606.5	67.3	164	1	DEST_MOUSE	O9r0p5 mus musculus

17	604.5	67.1	165	2	O6DV06	O6dv06 gekko japon
18	601.5	66.8	164	1	DEST_HUMAN	P60981 homo sapien
19	601.5	66.8	164	1	DEST_PIG	P60982 sus scrofa
20	598.5	66.4	164	2	O7M0E3	O7m0e3 rattus norv
21	392.5	43.6	163	2	O7ZWD8	O7zwd8 brachydanio
22	368.5	40.9	111	2	O8N1B5	O8n1b5 homo sapien
23	310.5	34.5	153	2	O7ZXD4	O7zxd4 xenopus lae
24	282.5	31.4	153	2	O6C0Y0	O6c0y0 yarrowia li
25	280	31.1	143	2	O9HF97	O9hf97 zygosacchar
26	276	30.6	143	2	O6BWX4	O6bwx4 debaryomyce
27	273	30.3	143	2	O6CQ22	O6cq22 kluyveromyce
28	271	30.1	143	2	O7S9P0	O7s9p0 ashbya goss
29	268	29.7	143	2	O9GVU9	O9gvu9 pichia angu
30	267.5	29.7	143	1	COF1_YEAST	Q03048 saccharomyc
31	265	29.4	143	2	O6FV81	O6fv81 candida gla
32	257.5	28.6	156	2	Q05307	Q05307 saccharomyc
33	257	28.5	137	1	ACTP_ACACA	P37167 acanthamoeb
34	254	28.2	137	1	COF1_SCHPO	P78929 schizosacch
35	230	25.5	137	1	COF1_DICDI	P54706 dictyostell
36	227.5	25.2	139	2	O6T8D2	O6t8d2 helianthus
37	227	25.2	139	1	ADF3_MAIZE	Q41764 zea mays (m
38	224.5	24.9	146	2	O8LCM6	O8lcm6 arabidopsis
39	222.5	24.7	463	2	O6JAG0	O6jag0 sorghum bic
40	220.5	24.5	139	1	ADF1_PETHY	O9fvi2 petunia hyb
41	220	24.4	140	2	O9M594	O9m594 elaeis guin
42	219.5	24.4	139	1	ADF1_ARATH	Q39250 arabidopsis
43	219.5	24.4	143	1	ADF2_PETHY	O9fvi1 petunia hyb
44	217.5	24.1	139	1	ADF4_ARATH	Q9zak3 arabidopsis
45	216	24.0	139	2	O84TE3	O84tb3 oryza sativ

ALIGNMENTS

RESULT 1
COF1_HUMAN STANDARD; PRT; 165 AA.
ID COF1_HUMAN AC P23528; O9UCA2;
DT 01-NOV-1991 (Rel. 20, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Cofilin, non-muscle isoform (Cofilin-1) (18 kDa phosphoprotein) (p18).
GN Name=COF1; Synonyms=CLF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91088330; PubMed=2263493;
RA Ogawa K., Tashima M., Yumoto Y., Okuda T., Sawada H., Okuma M.,
RA Maruyama Y.;
RT "Coding sequence of human placenta cofilin cDNA.";
RL Nucleic Acids Res. 18:7169-7169(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA der Steege G., Draaijers T.G., Grootsholten P.M., Osinga J.,
RA Anzevino R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,
RA Buys C.H.C.M.;
RN [3]
RP Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=96393653; PubMed=8800436;
RA Gillett G.T., Fox M.F., Rowe P.S.N., Casimir C.M., Povey S.;
RT "Mapping of human non-muscle type cofilin (COF1) to chromosome 11q13
and muscle type cofilin (COF2) to chromosome 14.";
RN Ann. Hum. Genet. 60:201-211(1996).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung, Ovary, Placenta, and Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 1-20.
RP TISSUE=Platelet;
RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
RA Thomas G.R., Vandekerckhove J.;
RT "Exploring proteomes and analyzing protein processing by mass
RT spectrometric identification of sorted N-terminal peptides.";
RL Nat. Biotechnol. 21:566-569(2003).
RN [6]
RP SEQUENCE OF 51-70.
RP TISSUE=Platelet;
RX MEDLINE=94311852; PubMed=8037689;
RA Davidson M.M., Haslam R.J.;
RT "Dephosphorylation of cofilin in stimulated platelets: roles for a
RT GTP-binding protein and C2+";
RL Biochem. J. 301:41-47(1994).
CC -1- FUNCTION: Controls reversibly actin polymerization and
CC depolymerization in a pH-sensitive manner. It has the ability to
CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
CC major component of intranuclear and cytoplasmic actin rods.
CC -1- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic; almost
CC completely in nucleus in cells exposed to heat shock or 10%
CC dimethyl sulfoxide.
CC -1- TISSUE SPECIFICITY: Widely distributed in various tissues.
CC -1- PTM: The phosphorylation of Ser-23 may prevent recognition of the
CC nuclear localization signal.
CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; D00682; BAA00589.1; -;
DR EMBL; U21909; AAB64501.1; -;
DR EMBL; X95404; CAA64685.1; -;
DR EMBL; BC011005; AAH11005.1; -;
DR EMBL; BC012265; AAH12265.1; -;
DR EMBL; BC012318; AAH12318.1; -;
DR EMBL; BC018256; AAH18256.1; -;
DR PIR; S12632; S12632.
DR HSSP; F18282; IAK6.
DR SWISS-2DPAGE; P23528; HUMAN.
DR Aarhus/Ghent-2DPAGE; 4; IEF.
DR OGP; P23528; -;
DR Genew; HGNC:1874; CFL1.
DR H-InVDB; HIX0009808; -;
DR MIM; 601442; -;
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; TAS.
DR GO; GO:0007266; P:Rho protein signal transduction; TAS.

DR InterPro; IPR002108; Actbind_coflin.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Actbind_coflin; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00345; ACTIN_DEPOLYMERIZING; 1.
KW Actin-binding; Cytoskeleton; Direct protein sequencing;
KW Nuclear protein; Phosphorylation.
FT INIT MET 0
FT DOMAIN 29 33 Nuclear localization signal (Potential).
FT DOMAIN 105 124 Actin-binding (Potential).
FT MOD_RES 23 23 Phosphoserine (Probable).
SQ SEQUENCE 165 AA; 18371 MW; EC9251A6D1C7C84C CRC64;
Alignment Scores:
Pred. No.: 2 38e-64 Length: 165
Score: 841.00 Matches: 165
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.34% Indels: 0
DB: 1 Gaps: 0
US-10-649-952a-2 (1-501) x COFI_HUMAN (1-165)
Qy 4 GCCTCCGGTGTGGCTGTCTCTGATGTGTCAAGGTGTCAACGACATGAAGTGCCT 63
Db 1 AlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysValArg 20
Qy 64 AGTCTTCAAGCCGAGAGGAGGTGAAGACGGCAAGAGCGGTGCTCTTCTGCTCAGT 123
Db 21 LysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeuSer 40
Qy 124 GAGGCAAGAAAGAACATCATCTGGAGGAGGCAAGAGAGATCTGTGGCGGATGTGGGC 183
Db 41 GluAspLysLysAsnIleIleLeuGluGluLysLysLysValGlyAspValGly 60
Qy 184 CAGACTGTTCGACGATCCCTACGCCACCTTTGTCAAGATGTGCCAGATAAGGACTGCCGC 243
Db 61 GlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCysArg 80
Qy 244 TATGCCCTCTATGATGCAACCTATGAGACCAAGAGAGCAAGAGGAGATCTGGTGT 303
Db 81 TyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuValPhe 100
Qy 304 ATCTTCTGGCCCGCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCCAGTCCCAAG 363
Db 101 IlePheThrAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSerLys 120
Qy 364 GAGCCATCAAGAAAGAGCTGACAGGGATCAAGCATGAATTGCAAGCAAACTGCTACGAG 423
Db 121 AspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyrGlu 140
Qy 424 GAGGTCAAGACCGCTGCACCCCTGGCGAGAGCAAGACTGGGGGGCAGTGGCGTCTCCTG 483
Db 141 GluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSerLeu 160
Qy 484 GAGGCGAAGCCTTTG 498
Db 161 GluGlyLysProLeu 165
RESULT 2
COFI_RAT
ID COFI_RAT STANDARD; PRT; 165 AA.
AC P45592;
DT 01-NOV-1995 (Rel. 32, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cofilin, non-muscle isoform (Cofilin-1).
GN Name=Cfli;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;

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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Wistar; TISSUE=Brain;
RL  Shiraawa T., Takahashi H., Sakamoto K., Kawashima A., Akashi T.;
RL  Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE, ACETYLATION, PHOSPHORYLATION SITE SER-23, AND MASS
RP  SPECTROMETRY.
RC  TISSUE=Parotid gland;
RA  Kanamori T., Suzuki M.M., Titani K.;
RT  "Complete amino acid sequences and phosphorylation sites, determined
RT  by Edman degradation and mass spectrometry, of rat parotid destrin-and
RT  cofilin-like protein.";
RL  Submitted (AUG-1998) to the PIR data bank.
CC  -1- FUNCTION: Controls reversibly actin polymerization and
CC  depolymerization in a pH-sensitive manner. It has the ability to
CC  bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
CC  major component of intranuclear and cytoplasmic actin rods (By
CC  similarity).
CC  -1- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By
CC  similarity).
CC  -1- TISSUE SPECIFICITY: Widely distributed in various tissues (By
CC  similarity).
CC  -1- PTM: The phosphorylation of Ser-23 may prevent recognition of the
CC  nuclear localization signal.
CC  -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
-----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
-----
DR  EMBL: X62908; CAA44694.1; --
DR  F01; S49101; S49101.
DR  HSP; P18282; IAK6.
DR  RGD; 69285; Cfil.
DR  InterPro: IPR002108; Actbind.cofil.
DR  Pfam: PF00241; Cofilin ADF; 1.
DR  PRINTS; PR00006; COFILIN.
DR  ProDom; PD002129; Actbind.cofil; 1.
DR  SMART; SM00102; ADF; 1.
DR  PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
KW  Acetylation; Actin-binding; Cytoskeleton; Direct protein sequencing;
KW  Nuclear protein; Phosphorylation.
FT  INIT MET 0 0
FT  MOD_RES 1 1 N-acetylalanine.
FT  DOMAIN 29 33 Nuclear localization signal (Potential).
FT  DOMAIN 105 124 Actin-binding (Potential).
FT  MOD_RES 23 23 Phosphoserine.
SQ  SEQUENCE 165 AA; 18401 MW; AD8FFACB671CA5E7 CRC64;

Alignment Scores:
Pred. No.: 5,29e-64 Length: 165
Score: 837,00 Matches: 164
Percent Similarity: 99,39% Conservative: 0
Best Local Similarity: 99,39% Mismatches: 1
Query Match: 92,90% Indels: 0
DB: 1 Gaps: 0

US-10-649-952a-2 (1-501) x COFI_RAT (1-165)

QY 4 GCCTCGGTGGCTGCTCTGATGGTGTTCATCAAGTGTTCACGACATGAAGTGGCT 63
Db 1 AlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysValArg 20
QY 64 AAGTCTTCAACGCCAGAGGAGGTGAAGAAGCGAAGGCGGTGCTCTTCTCGCTGAGT 123
Db 21 LysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeuSer 40
QY 124 GAGGACAAGAAGAACATCATCTCTGGAGGAGGAGGAGATCCTGTGGTGGCGATGTGGGC 183

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Db 41 GluAspLysLysAsnIleIleLeuGluGluGlyLysGluIleLeuValGlyAspValGly 60
QY 184 CAGACTGTTCGACGATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGCCGC 243
Db 61 GluThrValAspAspProTyrThrThrPheValLysMetLeuProAspLysAspCysArg 80
QY 244 TATGCCCTCTATGATGCAACCTATGAGACCAAGAGAGAGAGAGAGATCTGGTGT 303
Db 81 TyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuValPhe 100
QY 304 ATCTTCTGGCCCCCGAGCTGCGCCCTTAAGAGCAAAATGATTATGACGAGCTCAAG 363
Db 101 IlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSerLys 120
QY 364 GAGCCCATCAAGAAGAGCTGCAGGAGTCAAGCATGAATTGCAAGCAAACTGCTACGAG 423
Db 121 AspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyrGlu 140
QY 424 GAGGTCAAGGACCGCTGACCCCTGGCAGAGAACTGGGGGCGAGTGGCGTATCTCCCTG 483
Db 141 GluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSerLeu 160
QY 484 GAGGCGAAGCCTTTG 498
Db 161 GluGlyLysProLeu 165

RESULT 3
COFI_PIG STANDARD; PRT; 165 AA.
ID _COFI_PIG
AC P10668; Q29374;
DT 01-JUL-1989 (Rel. 11, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Cofilin, non-muscle isoform (Cofilin-1).
GN Names=CFIL1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=88298817; PubMed=3403546;
RA Matsuzaki F., Matsumoto S., Yahara I., Yonezawa N., Nishida E.,
RA Sakai H.;
RT "Cloning and characterization of porcine brain cofilin cDNA. Cofilin
RT contains the nuclear transport signal sequence.";
RL J. Biol. Chem. 263:11564-11568(1988).
RN [2]
RP SEQUENCE OF 1-103 FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=96327607; PubMed=8672129;
RA Winteroe A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RT library: analysis of 839 clones.";
RL Mamm. Genome 7:509-517(1996).
CC -1- FUNCTION: Controls reversibly actin polymerization and
CC depolymerization in a pH-sensitive manner. It has the ability to
CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
CC major component of intranuclear and cytoplasmic actin rods.
CC -1- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic; almost
CC completely in nucleus in cells exposed to heat shock or 10%
CC dimethyl sulfoxide.
CC -1- TISSUE SPECIFICITY: Widely distributed in various tissues.
CC -1- PTM: The phosphorylation of Ser-23 may prevent recognition of the
CC nuclear localization signal.
CC -1- MISCELLANEOUS: A double mutation of Lys-111 and Lys-113 to Gln
CC produces a mutant with no ability to depolymerize or bind F-actin.
CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
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DR EMBL; M20866; AAA31020.1; -;
 DR EMBL; F14577; CAA23134.1; -;
 DR PIR; A29240; A29240.
 DR HSPF; F18282; 1AK6.
 DR InterPro; IPR002108; Actbind_coflin.
 DR Pfam; PF00241; Cofilin_ADF; 1.
 DR PRINTS; PR00006; COFILIN.
 DR ProDom; PD002129; Actbind_coflin; 1.
 DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
 KW Actin-binding; Cytoskeleton; Direct protein sequencing;
 KW Nuclear protein; Phosphorylation.
 FT INIT MET 0 By similarity.
 FT DOMAIN 29 33 Nuclear localization signal (Potential).
 FT DOMAIN 105 124 Actin-binding (Potential).
 FT MOD_RES 23 23 Phosphoserine (By similarity).
 FT MUTAGEN 111 111 K->Q: Slight modification of activity.
 FT MUTAGEN 113 113 K->Q: Impairs interaction with actin.
 SQ SEQUENCE 165 AA; 18387 MW; EC9241B6D1D7D84C CRC64;

Alignment Scores:
 Pred. No.: 6.46e-64 Length: 165
 Score: 836.00 Matches: 164
 Percent Similarity: 99.39% Conservative: 0
 Best Local Similarity: 99.39% Mismatches: 1
 Query Match: 92.79% Indels: 0
 DB: 1 Gaps: 0

US-10-649-952A-2 (1-501) x COFI_PIG (1-165)

QY 4 GCCTCCGGTGGTGTCTCTGATGGTCTCATCAAGGTGTTCAACGACATGAAGTGGT 63
 DB 1 AlaserGlyValAlaValSerAspGlyValIleValPheAsnAspMetLysValArg 20
 QY 64 AAGTCTTCAACGCCAGGAGGTGAAGAGCGGCGGTCTCTTCTGCTCGT 123
 DB 21 LysSerSerThrProGluGluValLysArgLysLysAlaValLeuPheCysLeuSer 40
 QY 124 GAGCAACAAGAACATCATCTCGAGGAGCGGAGGATCTCGTGGCGATGGGC 183
 DB 41 GluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspValGly 60
 QY 184 CAGACTGTGACGATCCCTACGACCTTTCTCAAGATGCTGCCAGATAAGGACTGCCGC 243
 DB 61 GinThrValAspAspProTyAlaThrPheValLysMetLeuProAspLysAspCysArg 80
 QY 244 TATGCCCTCTATGATCAACCTATGACACCAAGGAGGAGGAGGATCTCGTGT 303
 DB 81 TyrAlaLeuTyAspAlaThrTy-GluThrLysGluSerLysLysGluAspLeuValPhe 100
 QY 304 ATCTTCTGGGCCCCGAGCTGCGCCCTTAAGAGCAAAATGATTATGCCAGCTCCAAG 363
 DB 101 IlePheTrpAlaProGluCysAlaProLeuLysSerLysMetIleTyAlaSerSerLys 120
 QY 364 GACGCCATCAAGAAGAGCTCACAGGGATCAAGATGAATTCGAAGCAAACTGTACGAG 423
 DB 121 AspalalleLysLysLeuThrGlyLysHisGluLeuGlnAlaAsnCytyGlu 140
 QY 424 GAGGTCAAGGACCGCTGCACCTCGCAGAGAGCTGGGGGCGAGTGGCGTTCATCTCCCTG 483
 DB 141 GluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSerLeu 160
 QY 484 GAGGCAAGCCTTTG 498
 DB 161 GluGlyLysProLeu 165

RESULT 4

COFI_SHEEP
 ID COFI_SHEEP STANDARD; PRT; 165 AA.
 AC Q657M7; 2004 (Rel. 45, Created)
 DT 25-OCT-2005 (Rel. 46, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DB Cofilin, non-muscle isoform (Cofilin-1).
 GN Name=COFIL1; (Sheep).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Endometrium;
 RA Welker J.E., Ott T.L.;
 RT "Cloning and characterization of cofilin-1 expression in cyclic and
 RT early pregnant ovine endometrium following isolation by yeast-two
 RT hybrid screening";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Controls reversibly actin polymerization and
 CC depolymerization in a pH-sensitive manner. It has the ability to
 CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
 CC major component of intranuclear and cytoplasmic actin rods (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By
 CC similarity).
 CC -!- PTM: The phosphorylation of Ser-23 may prevent recognition of the
 CC nuclear localization signal (By similarity).
 CC -!- SIMILARITY: Belongs to the actin-binding proteins ADF family.
 CC
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DR EMBL; AY676116; AAT77679.1; -;
 DR ProDom; PD002129; Actbind_coflin; 1.
 DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
 KW Actin-binding; Cytoskeleton; Nuclear protein; Phosphorylation.
 FT INIT_MET 0 By similarity.
 FT DOMAIN 29 33 Nuclear localization signal (Potential).
 FT DOMAIN 105 124 Actin-binding (Potential).
 FT MOD_RES 23 23 Phosphoserine (By similarity).
 SQ SEQUENCE 165 AA; 18387 MW; EC9241B6D1D7D84C CRC64;

Alignment Scores:
 Pred. No.: 6.46e-64 Length: 165
 Score: 836.00 Matches: 164
 Percent Similarity: 99.39% Conservative: 0
 Best Local Similarity: 99.39% Mismatches: 1
 Query Match: 92.79% Indels: 0
 DB: 1 Gaps: 0

US-10-649-952A-2 (1-501) x COFI_SHEEP (1-165)

QY 4 GCCTCCGGTGGTGTCTCTGATGGTCTCATCAAGGTGTTCAACGACATGAAGTGGT 63
 DB 1 AlaserGlyValAlaValSerAspGlyValIleValPheAsnAspMetLysValArg 20
 QY 64 AAGTCTTCAACGCCAGGAGGTGAAGAGCGGCGGTCTCTTCTGCTCGT 123
 DB 21 LysSerSerThrProGluGluValLysArgLysLysAlaValLeuPheCysLeuSer 40
 QY 124 GAGCAACAAGAACATCATCTCGAGGAGCGGAGGATCTCGTGGCGATGGGC 183
 DB 41 GluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspValGly 60
 QY 184 CAGACTGTGACGATCCCTACGACCTTTCTCAAGATGCTGCCAGATAAGGACTGCCGC 243
 DB 61 GinThrValAspAspProTyAlaThrPheValLysMetLeuProAspLysAspCysArg 80
 QY 244 TATGCCCTCTATGATCAACCTATGACACCAAGGAGGAGGAGGATCTCGTGT 303
 DB 81 TyrAlaLeuTyAspAlaThrTy-GluThrLysGluSerLysLysGluAspLeuValPhe 100
 QY 304 ATCTTCTGGGCCCCGAGCTGCGCCCTTAAGAGCAAAATGATTATGCCAGCTCCAAG 363
 DB 101 IlePheTrpAlaProGluCysAlaProLeuLysSerLysMetIleTyAlaSerSerLys 120
 QY 364 GACGCCATCAAGAAGAGCTCACAGGGATCAAGATGAATTCGAAGCAAACTGTACGAG 423
 DB 121 AspalalleLysLysLeuThrGlyLysHisGluLeuGlnAlaAsnCytyGlu 140
 QY 424 GAGGTCAAGGACCGCTGCACCTCGCAGAGAGCTGGGGGCGAGTGGCGTTCATCTCCCTG 483
 DB 141 GluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSerLeu 160
 QY 484 GAGGCAAGCCTTTG 498
 DB 161 GluGlyLysProLeu 165

Db 61 GlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCysArg 80
 QY 244 TATGCGCTCTATGATCAACTATGACACCAAGGAGAGGAGGATCTGGTGT 303
 Db 81 TyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysGluAspLeuValPhe 100
 QY 304 ATCTTCTGGCCCCGAGTCTGGCCCTTAAAGAGCAAAATGATTATTCAGCTCCAAG 363
 Db 101 IlePheTrpAlaProGluCysAlaProLeuLysSerLysMetIleTyrAlaSerSerLys 120
 QY 364 GAGCCATCAAGAGAGCTGACAGGATCAAGCATCAATGCAAGCAAACTCTACGAG 423
 Db 121 AspAlaIleLysLysLysLeuThrGlyLeuHisGluLeuGlnAlaAsnCysTyrGlu 140
 QY 424 GAGGTCAAGCAGCTGCGAGAGAGCTGGGCGGAGAGCTGGGCGGAGTGGGGTCACTCCCTG 483
 Db 141 GluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSerLeu 160
 QY 484 GAGGGCAAGCTTTG 498
 Db 161 GluGlyLysProLeu 165

RESULT 5

COPI_MOUSE STANDARD; PRT; 165 AA.
 AC P18760;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 25-JAN-2005 (Rel. 46, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Cofilin, non-muscle isoform (Cofilin-1).
 GN Names=Cfil1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss Webster;
 RX MEDLINE=90272419; PubMed=2349104;
 RA Moriyama K., Matsumoto S., Nishida E., Sakai H., Yahara I.;
 RT "Nucleotide sequence of mouse cofilin cDNA."
 RL Nucleic Acids Res. 18:3053-3053(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins L.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.W., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Mutsaers J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Controls reversibly actin polymerization and
 depolymerization in a pH-sensitive manner. It has the ability to
 bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
 major component of intranuclear and cytoplasmic actin rods.
 CC -1- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic; almost
 completely in nucleus in cells exposed to heat shock or 10%

dimethyl sulfoxide.
 CC -1- TISSUE SPECIFICITY: Widely distributed in various tissues.
 CC -1- PTM: The phosphorylation of Ser-23 may prevent recognition of the
 nuclear localization signal.
 CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; D00472; BAA00364.1; -;
 DR EMBL; BC058726; AAH58726.1; -;
 DR PIR; S12584; S12584.
 DR KSSP; P18282; IAK6.
 DR SWISS-2DPAGE; P18760; MOUSE.
 DR MGD; MGI:101757; Cfil1.
 DR InterPro; IPR002108; Actbind cofln.
 DR Pfam; PF00241; Cofilin ADF; 1.
 DR PRINTS; PR00006; COFILIN.
 DR ProDom; PD002129; Actbind cofln; 1.
 DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
 KW Actin-binding; Cytoskeleton; Nuclear protein; Phosphorylation.
 FT INIT MET 0 0 By similarity.
 FT DOMAIN 29 33 Nuclear localization signal (Potential).
 FT DOMAIN 105 124 Actin-binding (Potential).
 FT MOD_RES 23 23 Phosphoserine (By similarity).
 SQ SEQUENCE 165 AA; 18428 MW; AD8FE7D66701B8E7 CRC64;
 Alignment Scores:
 Pred. No.: 9 63e-64 Length: 165
 Score: 834.00 Matches: 163
 Percent Similarity: 99.39% Conservative: 1
 Best Local Similarity: 98.79% Mismatches: 1
 Query Match: 92.56% Indels: 0
 DB: 1 Gaps: 0
 US-10-649-952A-2 (1-501) x COPI_MOUSE (1-165)

QY 4 GCCTCCGTTGCTCTCTCTGATGCTCATCAAGGTGTTCACGATGTTCAACGATGAAGTGCCT 63
 Db 1 AlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysValArg 20
 QY 64 AGTCTTCAAGCCAGAGAGGAGTGAAGAGCGGAGAGCGGTCTCTTCCTCCTGAGT 123
 Db 21 LysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeuSer 40
 QY 124 GAGGACAAAGAACATCATCTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 183
 Db 41 GluAspLysLysAsnIleLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGly 60
 QY 184 CAGACTGTGCGAGATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATGAAGGATCCCGC 243
 Db 61 GlnThrValAspAspProTyrThrThrPheValLysMetLeuProAspLysAspCysArg 80
 QY 244 TATGCCCTCTATGATGCAACCTATGAGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 303
 Db 81 TyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuValPhe 100
 QY 304 ATCTTCTGGCCCCGAGTCTGGCCCTTAAAGAGCAAAATGATTATTCAGCTCCAAG 363
 Db 101 IlePheTrpAlaProGluAsnAlaProLeuLysSerLysMetIleTyrAlaSerSerLys 120
 QY 364 GAGCCATCAAGAGAGCTGACAGGATCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCA 423
 Db 121 AspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyrGlu 140
 QY 424 GAGGTCAAGAGCGCTGACCCCTGGCAGAGAGCTGGGGGGGAGTCCGGTCACTCCCTG 483
 Db 141 GluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSerLeu 160

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Qy 484 GAGGCAAGCCTTGTG 498
Db 161 GluGlyLysProLeu 165

RESULT 6
Q9CX22 PRELIMINARY; PRT; 229 AA.
AC Q9CX22;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 12 days embryo embryonic body between diaphragm region
DE and neck cDNA, RIKEN full-length enriched library, clone:9430060J01
DE product:cofilin 1, non-muscle, full insert sequence.
GN Name=Cfil;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX RIKEN FANTOM Consortium;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX RIKEN FANTOM Consortium;
RA "Analysis of the mouse transcriptome based on functional annotation of
  60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RC MEDLINE=20493174; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
  Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RA "Normalization and subtraction of cap-trapper-selected cDNAs to
  prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
  Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
  Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
  Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
  Fujiwaka S., Inoue K., Togawa Y., Iizawa M., Ohara E., Watahiki M.,
  Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
  Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
  sequencing pipeline with 384 multipipillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;

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RC TISSUE=Embryonic body between diaphragm region and neck;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK020471; BAB32114.1; -
DR HSSP; P60982; IAK6
DR MGD; MGI:101757; Cfil.
DR GO; GO:0030864; C:cortical actin cytoskeleton; IDA.
DR InterPro; IPR002108; Actbind_cofln.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Actbind_cofln; 1.
DR SMART; SMO0102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
SQ SEQUENCE 229 AA; 24795 MW; 1198EAA88F166B75 CRC64;

Alignment Scores:
Pred. No.: 1.82e-63 Length: 229
Score: 831.00 Matches: 162
Percent Similarity: 99.39% Conservative: 2
Best Local Similarity: 98.18% Mismatches: 1
Query Match: 92.23% Indels: 0
DB: 2 Gaps: 0

US-10-649-952A-2 (1-501) x Q9CX22 (1-229)
Qy 1 ATGCGCTCCGGTGTGGCTGTCTCTGTATGTTTCATCAAGGTGTTCAACGACATGAAGTG 60
Db 1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAenAspMetLysVal 20
Qy 61 CGTAAGTCTTCAAGCCAGAGGAGGTGAAGAGGGCAAGAGGGGGTCTCTTCGCTG 120
Db 21 ArgLysSerSerThrProGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
Qy 121 AGTGAGGACAAAGAAACATCATCTCGAGGAGGCAAGAGATCTCTGGTGGCGATGTG 180
Db 41 SerGluAspLysLysAsnIleLeuGluGluLysLysLysLysLysLysValGlyAspVal 60
Qy 181 GGCACAGACTGTGACGATCCCTACGCCACCTTTTGTCAAGATGCTCCAGATAAGGACTGC 240
Db 61 GlyGlnThrValAspAspProTyThrThrPheValLysMetLeuProAspLysAspCys 80
Qy 241 CGCTATGCCCTCTATGATGCAACCTATGAGACCCAGAGAGAGAGAGAGGATCTGGTG 300
Db 81 ArgTyraLeuLeuTyraAspAlaThrTyraGluThrLysGluSerLysLysGluAspLeuVal 100
Qy 301 TTTATCTTCTGGGCCCCCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCCAGCTCC 360
Db 101 PheIlePheIraProGluAsnAlaProLeuLysSerLysMetIleTyraLysSer 120
Qy 361 AAGGACCCCATCAAGAAAGAGCTGACAGGGATCAAGGATCAATTCGAAGCAAACTGTAC 420
Db 121 LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAenCysTyr 140
Qy 421 GAGGAGTCAAGAGCCCTGCACCTCGAGAGAGAGCTGGGGGGCAGTGGGGTCTATCC 480
Db 141 GluLysValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer 160
Qy 481 CTGAGGGGCAAGCCT 495
Db 161 LeuGluGlyLysPro 165

RESULT 7
COFI_CHK

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ID AC P21566; STANDARD; PRT; 166 AA.
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cofilin.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=91027755; PubMed=1699599;
 RA Abe H., Endo T., Yamamoto K., Ohinata T.;
 RT "Sequence of cDNAs encoding actin depolymerizing factor and cofilin of
 RT embryonic chicken skeletal muscle: two functionally distinct actin-
 RT regulatory proteins exhibit high structural homology.";
 RL Biochemistry 29:7420-7425 (1990).
 RN [2]
 RP STRUCTURE BY NMR, AND REVISIONS TO 53-54.
 RX MEDLINE=21880669; PubMed=11885570; DOI=10.1014/227808686;
 RA Bains N.P.S., Gorbatyuk V.Y., Neworthy N.J., Robson S.A.,
 RA Maciejewski M.W., dos Remedios C.G., King G.P.;
 RT "Backbone and side-chain 1H, 15N, and 13C assignments for chick
 RT cofilin.";
 RL J. Biomol. NMR 22:193-194 (2002).
 CC -I- FUNCTION: Controls reversibly actin polymerization and
 CC depolymerization in a pH-sensitive manner. It has the ability to
 CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
 CC major component of intranuclear and cytoplasmic actin rods.
 CC -I- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic; almost
 CC completely in nucleus in cells exposed to heat shock or 10%
 CC dimethyl sulfoxide.
 CC -I- TISSUE SPECIFICITY: Widely distributed in various tissues.
 CC -I- PTM: The phosphorylation of Ser-24 may prevent recognition of the
 CC nuclear localization signal.
 CC -I- SIMILARITY: Belongs to the actin-binding proteins ADF family.
 CC
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 CC
 CC EMBL; M55659; AAA62732.1; -;
 DR HSSP; P18282; 1AK6.
 DR InterPro; IPR002108; Actbind cofilin.
 DR Pfam; PF00241; Cofilin ADF; 1.
 DR PRINTS; PR00006; COFILIN
 DR ProDom; PD002129; Actbind_cofilin; 1.
 DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
 KW Actin-binding; Cytoskeleton; Nuclear protein; Phosphorylation.
 FT DOMAIN 30 34 Nuclear localization signal (Potential).
 FT DOMAIN 106 125 Actin-binding (Potential).
 FT MOD_RES 24 24 Phosphoserine (By similarity).
 SQ SEQUENCE 166 AA; 18661 MW; 514685E940786BF0 CRC64;
 Alignment Scores:
 Pred. No.: 6 81e-53 Length: 166
 Score: 709.00 Matches: 136
 Percent Similarity: 89.76% Conservative: 13
 Best Local Similarity: 81.93% Mismatches: 17
 Query Match: 78.69% Indels: 0
 DB: 1 Gaps: 0

US-10-649-952A-2 (1-501) x COFI_CHICK (1-166)

QY 1 ATGGCTCGGTGGCTGTCTGTGATGGTGTATCAAGGTGTTCACGACATGAAGGTG 60

Db 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20
 QY 61 CGTAAGTCTTCAACGCGCAGAGGAGTGAAGACGCAAGAGCGGTCTCTTCTGCTG 120
 Db 21 ArgLysSerSerThrProGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40
 QY 121 AGTGAGGCAAGAAACATCATCTCTGGAGGAGGCAAGAGATCTCTGTGGCGGATGTG 180
 Db 41 SerAspLysLysGlnIleValGluAlaLysGlnIleLeuValGlyAspIle 60
 QY 181 GGCCAGACTGTGACCATCCCTACGCCCTTTGTCAAGATGCTGCAGATAGGACTGC 240
 Db 61 GlyAspThrValGluAspProTyrThrAlaPheValLysLeuLeuProLeuAsnAspCys 80
 QY 241 CGTATGCTCTTATCATGCACTATGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
 Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
 QY 301 TTTATCTTGGGCCCCCGAGTCTGCGCCCTTAAAGCAAAATGATTATTCAGCTCC 360
 Db 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
 QY 361 AAGGAGCCATCAAGAGAGCTGACAGGATCAACATGATTCGACCAACTGCTAC 420
 Db 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHieGluTrpGlnValAsnGlyLeu 140
 QY 421 GAGGAGGTCAAGGACGCTGCACCCCTGGCAGAGAACTGGGGCGCAGTGGCGTCATCTCC 480
 Db 141 AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyValValSer 160
 QY 481 CTGGAGGGCAAGCCTTTG 498
 Db 161 LeuGluGlyLysProLeu 166
 RESULT 8
 COF2_MOUSE
 ID COF2_MOUSE STANDARD; PRT; 166 AA.
 AC P45531;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Cofilin, muscle isoform (Cofilin-2).
 GN Names=Cfil2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H; TISSUE=Skeletal muscle;
 RX MEDLINE=94253093; PubMed=8195165;
 RA Ono S., Minami N., Abe H., Ohinata T.;
 RT "Characterization of a novel cofilin isoform that is predominantly
 RT expressed in mammalian skeletal muscle.";
 RL J. Biol. Chem. 269:15280-15286 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Controls reversibly actin polymerization and
 CC depolymerization in a pH-sensitive manner. It has the ability to
 CC bind G- and F-actin in a 1:1 ratio of cofillin to actin. It is the
 CC major component of intranuclear and cytoplasmic actin rods.
 CC -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in skeletal muscle.
 CC -!- PTM: The phosphorylation of Ser-24 may prevent recognition of the
 CC nuclear localization signal.
 CC -!- SIMILARITY: Belongs to the actin-binding proteins ADF family.
 CC -----
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 CC -----
 DR EMBL; L29468; AAA37433.1; --
 DR EMBL; BC007138; AAH07138.1; --
 DR PIR; A53812; A53812.
 DR HSP; P18282; IAK6.
 DR MGD; MGI:101763; Cf12.
 DR InterPro; IPR002108; Actbind_coflin.
 DR Pfam; PF00241; Cofilin_ADF; 1.
 DR PRINTS; PR00006; COFILIN.
 DR PRODOM; PD002129; Actbind_coflin; 1.
 DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
 KW Actin-binding; Cytoskeleton; Nuclear localization signal (Potential).
 FT DOMAIN 30 34
 FT DOMAIN 106 125 Actin-binding (Potential).
 FT MOD RES 24 24 Phosphoserine (By similarity).
 SQ SEQUENCE 166 AA; 18709 MW; 486D7E5AE9FE1CC CRC64;
 Alignment Scores:
 Pred. No.: 2,76e-52 Length: 166
 Score: 702.00 Matches: 135
 Percent Similarity: 89.76% Conservative: 14
 Best Local Similarity: 81.33% Mismatches: 17
 Query Match: 77.91% Indels: 0
 DB: 1 Gaps: 0
 US-10-649-952A-2 (1-501) x COF2_MOUSE (1-166)
 Qy 1 ATGCGCTCGGTGGCTGCTCTGATGGTGTCTCAAGGTTTCACGACATGAAGTG 60
 Db 1 MetalaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20
 Qy 61 CGTAAGCTTCAACGCCAGAGAGGTGAAGAGCGCAAGAGCGGCTCTTCGCTG 120
 Db 21 ArgLysSerThrGlnGluGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40
 Qy 121 AGTGAGGACAGAAAGAACATCATCTCGAGAGGCGCAAGAGATCTCTGGTGGCGATGTG 180
 Db 41 SerAspAspLysArgGlnIleValGluGluAlaLysGlnIleLeuValGlyAspIle 60
 Qy 181 GCCGAGACTGTGAGAGTCCCTACGCCACCTTTGTCAGATGCTGCCAGATAAGGATGCG 240
 Db 61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 80
 Qy 241 CGCTATCCCTCTATGCAACCTATCAGACCAAGAGGAGGACAGAGGAGGATCTGGTG 300
 Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
 Qy 301 TTTATCTTCTGGGCCCGCCGAGTCTGCGCCCTTAAAGAGCAAAATGATTATGCGAGCTCC 360

Db 101 PheilePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
 Qy 361 AAGGACCCCATCAAGAGAGAGCTGACAGGATCATGAGCATGAATGCGCAAACTGCTAC 420
 Db 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 140
 Qy 421 GAGGAGGTCAAGGACCCCTGCACCTCGGACAGAAAGCTGGGGGCGACGTGCGGTCTATCTCC 480
 Db 141 AspAspIleLysAspArgSerThrLeuGlyLysLeuGlyLysValValValSer 160
 Qy 481 CTGAGGCGCAAGCCTTTG 498
 Db 161 LeuGluGlyLysProLeu 166
 RESULT 9
 COF2 HUMAN STANDARD; PRT; 166 AA.
 ID COF2 HUMAN AC Q9Y2B1;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Cofilin, muscle isoform (Cofilin-2).
 GN Name=CFL2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jin J., Li G., Hu S., Li W., Yuan J., Qiang B.;
 RT "Isolation of two isoforms of human cofilin cDNA";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21315834; PubMed=11422377;
 RA Thirion C., Stucka R., Mendel B., Gruhler A., Jaksch M., Nowak K.J.,
 RA Binz N., Laing N.G., Lochmuller H.;
 RT "Characterization of human muscle type cofilin (CFL2) in normal and
 RT regenerating muscle.";
 RL Eur. J. Biochem. 268:3473-3482(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RT TISSUE=Bone marrow, Placenta, and Skeletal muscle;
 RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Controls reversibly actin polymerization and
 CC depolymerization in a pH-sensitive manner. It has the ability to
 CC bind G- and F-actin in a 1:1 ratio of cofillin to actin. It is the
 CC major component of intranuclear and cytoplasmic actin rods (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By
 CC similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;

CC Comment-Isoforms are identical at the level of the protein
 CC sequence;
 CC Names=CFL2b;
 CC IsoId=Q9Y281-1; Sequence=Displayed;
 CC Name=CFL2a;
 CC IsoId=Q9Y281-2; Sequence=Not described;
 CC -1- TISSUE SPECIFICITY: Isoform CFL2b is expressed predominantly in
 CC skeletal muscle and heart, while isoform CFL2a is expressed in
 CC various tissues.
 CC -1- PTM: The phosphorylation of Ser-24 may prevent recognition of the
 CC nuclear localization signal.
 CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC ENBL; AF134802; AAD31280.1; -;
 CC ENBL; AF134803; AAD31281.1; -;
 CC ENBL; AF283513; AAF97934.1; -;
 CC ENBL; AF242299; AAF64498.1; -;
 CC ENBL; BC011444; AAH11444.1; -;
 CC ENBL; BC022364; AAH22364.1; -;
 CC ENBL; BC022876; AAH22876.1; -;
 CC HSP; P18282; IAK6.
 CC Genew; HGNC:1875; CFL2.
 CC MIM; 601443; -;
 CC InterPro; IPR002108; Actbind_cofin.
 CC Pfam; PF00241; Cofilin_ADF; 1.
 CC PRINTS; PR00006; COFILIN.
 CC ProDom; PD002129; Actbind_cofin; 1.
 CC SMART; SM00102; ADF; 1.
 CC PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
 CC Actin-binding; Alternative splicing; Cytoskeleton; Nuclear protein;
 CC Phosphorylation.
 CC DOMAIN 30 34 Nuclear localization signal (Potential).
 CC FT DOMAIN 106 125 Actin-binding (Potential).
 CC FT MOD_RES 24 24 Phosphoserine (By similarity).
 CC SQ SEQUENCE 166 AA; 18736 MW; 48B6DCCAE9FE1CC CRC64;
 Alignment Scores:
 Pred. No.: 5.03e-52 Length: 166
 Score: 699.00 Matches: 134
 Percent Similarity: 89.76% Conservative: 15
 Best Local Similarity: 80.72% Mismatches: 17
 Query Match: 77.58% Indels: 0
 DB: 1 Gaps: 0
 US-10-649-952a-2 (1-501) x COP2_HUMAN (1-166)
 QY 1 ATGGCTTCGGTGGCTGCTCTGATGCTCATCAAGGTGTCAACGACATGAAGGTG 60
 DB 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20
 QY 61 CGTAAGTCTTCAAGCGGAGGAGGTGAGCAAGCGGAGGAGGCTGCTCTGCTG 120
 DB 21 ArgLysSerSerThrGlnGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40
 QY 121 AGTGAGGACAAAGAAACATCATCTCGAGGAGGCAAGAGAGATCTGTGGGCGATG 180
 DB 41 SerAspAspLysArgGlnIleIleValGluGluAlaLysGlnIleLeuValGlyAspIle 60
 QY 181 GGCGACAGTGTGACGATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
 DB 61 GlyAspThrValGluAspProTyrThrSerPheValIleLeuLeuProLeuAsnAspCys 80
 QY 241 CGCTATGCTCTATGATGCAACTATGAGACCAAGAGAGGAGGAGGATCTGGTG 300
 DB 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100

QY 301 TTTATCTTCTGGCCCCCGAGTCTGGCCCTTTAAGAGCAAAATGATTTATGCAGCTCC 360
 DB 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
 QY 361 AAGGAGCCATCAAGAAGAGCTGACAGGATCAAGCATGAATTCAGCAAACTGCTAC 420
 DB 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 140
 QY 421 GAGGAGGTCAAGGACCGCTGCACCTGGCAGAGAAGCTGGGGGCGAGTGGGTCATCTCC 480
 DB 141 AspAspIleLysAspArgSerThrLeuGlyLysLeuGlyLysValValSer 160
 QY 481 CTGGAGGGCAAGCCTTTG 498
 DB 161 LeuGluGlyLysProLeu 166
 RESULT 10
 Q6NZW3 PRELIMINARY; PRT; 166 AA.
 AC Q6NZW3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cofilin 2 (Muscle).
 GN Name=CFL2;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RC TISSUE=Embryo;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zdobych B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Director MGC Project;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC065947; AAH65947.1; -;
 DR HSSP; P60982; IAK6.
 DR ZFIN; ZDB-GENE-040426-1815; cfl2.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003779; F:actin binding; IEA.
 DR InterPro; IPR002108; Actbind_cofln.
 DR Pfam; PF00241; Cofilin_ADF; 1.
 DR PRINTS; PR00006; COFILIN.
 DR ProDom; PD002129; Actbind_cofln; 1.
 DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
 DR SEQUENCE 166 AA; 18568 MW; 795942E0F8F0A2D6 CRC64;

Alignment Scores:

Pred. No.: 1.67e-51 Length: 166
 Score: 693.00 Matches: 133
 Percent Similarity: 89.76% Conservative: 16
 Best Local Similarity: 80.12% Mismatches: 17
 Query Match: 76.91% Indels: 0
 DB: 2 Gaps: 0

US-10-649-952A-2 (1-501) x Q6NZW3 (1-166)

QY 1 ATGGCTCGGTGGTGGTCTCTGATGTCATCAAGGTGTTCAACGACATGAAGTGTG 60
 Db 1 MetAlaSerGlyValThrValSerAspGluValIleLysValPheAsnAspMetLysVal 20
 QY 61 CGTAAAGTCTTCAACGCCAGAGAGAGTGAAGAGCGCAGAGAGCGGTGCTCTCTGCTGTG 120
 Db 21 ArgLysSerSerSerSerAspGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
 QY 121 AGTGAGGACAAAGAACATCATCTCGAGGAGGCGCAAGGAGATCCTGGTGGCGATGTG 180
 Db 41 SerAspAspLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 60
 QY 181 GCGCAGACTGTCAGGATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGACTGTC 240
 Db 61 GlyAspSerValAspAspProTyrAlaCysPheValLysLeuLeuProLeuAsnAspCys 80
 QY 241 CGCTATGCTCTATGATGCAACCTATGAGACCAAGGAGGAGCAAGGAGGATCTGGTG 300
 Db 81 ArgTyrGlyLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysLysLysLysLys 100
 QY 301 TTTATCTTCTGGGCCCCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCGAGTCTCC 360
 Db 101 PheIlePheTyrAlaProGluGlyAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
 QY 361 AAGGAGCGCATCAAGAGAGCTGACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
 Db 121 LysAspAlaIleLysLysLysPheThrGlyIleLysLysLysLysLysLysLysLysLys 140
 QY 421 GAGGAGGTCAAGGACCGTGCACCTGCGACGAGAGTGGGGGCGAGTGGCGTATCTCC 480
 Db 141 AspAspIleGlnAspArgSerThrLeuAlaGluLysLeuGlyGlyAsnValValSer 160
 QY 481 CTGGAGGCGCAAGCCTTTG 498
 Db 161 LeuGluGlyArgProLeu 166

RESULT 11

Q6NX11 PRELIMINARY; PRT; 168 AA.
 AC Q6NX11;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DE Hypothetical protein MGC76274.
 GN Name=MGC76274;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8364;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marta M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Gerhard D.S.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC067328; AAH67328.1; -.
 DR HSSP; P60982; IAK6.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003779; F:actin binding; IEA.
 DR InterPro; IPR002108; Actbind_cofin.
 DR Pfam; PF00241; Cofilin_ADF; 1.
 DR PRINTS; PR00006; COFILIN.
 DR ProDom; PD002129; Actbind_cofin; 1.
 DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
 DR Hypothetical protein.
 SQ SEQUENCE 168 AA; 19073 MW; 14AB09FF9616496A CRC64;

Alignment Scores:

Pred. No.: 1.49e-48 Length: 168
 Score: 659.00 Matches: 130
 Percent Similarity: 83.13% Conservative: 8
 Best Local Similarity: 78.31% Mismatches: 28
 Query Match: 73.14% Indels: 0
 DB: 2 Gaps: 0

US-10-649-952A-2 (1-501) x Q6NX11 (1-168)

QY 1 ATGGCTCGGTGGTGGTCTCTGATGTCATCAAGGTGTTCAACGACATGAAGTGTG 60
 Db 1 MetAlaSerGlyValMetValSerAspValLysValPheAsnAspMetLysVal 20
 QY 61 CGTAAAGTCTTCAACGCCAGAGGAGTGAAGAGCGCAGAGGCGGTGCTCTCTGCTGTG 120
 Db 21 ArgHisGlnLeuSerProGluGluAlaLysLysArgLysLysAlaValValPheCysLeu 40
 QY 121 AGTGAGGACAAAGAACATCATCTCGAGGAGGCGCAAGGAGATCCTGGTGGCGATGTG 180
 Db 41 SerGluAspLysLysMetIleLeuGluProGlyLysLysLysLysLysLysLysLysLys 60
 QY 181 GCGCAGACTGTCAGCATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGACTGTC 240
 Db 61 GlyCysAsnValAspAspProTyrLysAlaPheValLysMetLeuProArgAsnAspCys 80
 QY 241 CGCTATGCTCTATGATGCAACCTATGAGACCAAGGAGGAGCAAGGAGGATCTGGTG 300
 Db 81 ArgTyrAlaLeuTyrAspAlaLeuTyrGluThrLysGluThrLysLysGluAspLeuVal 100
 QY 301 TTTATCTTCTGGGCCCCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCGAGTCTCC 360
 Db 101 PheValPheTyrAlaProGluGluAlaSerLeuLysSerLysMetIleTyrAlaSerSer 120
 QY 361 AAGGAGCGCATCAAGAGAGCTGACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
 Db 121 LysAspAlaIleLysLysLysPheThrGlyIleLysLysLysLysLysLysLysLysLys 140
 QY 421 GAGGAGGTCAAGGACCGTGCACCTGCGACGAGAGTGGGGGCGAGTGGCGTATCTCC 480
 Db 141 GluAspIleAsnAspProCysAsnLeuAlaGluLysLeuGlyGlySerThrValIleSer 160
 QY 481 CTGGAGGCGCAAGCCTTTG 498
 Db 161 LeuGluGlyArgProLeu 166

Qy		1 ATGCGCTCCGGTGGCTGTCTTGATGGTGTCATCAAGGTGTTCAACGACATGAAGGTG 60
Db		1 MetAlaSerGlyValMetValSerAspValVallysValpheAsnAspMetylSval 20 ::

Song H.D., Wu X.Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
Sheng Y., Chen Y., Ruan Z., Jiang C.L., Fan H.Y., Zou L.I.,
Kanki J.P., Look A.T., Chen Z.,
Submitted (SEP-2003) to the EMBL/GenBank/DBAJ databases.
EMBL: AY398324; AAQ97757.1; -.
DR HSP; P60982; IAK6.
DR ZFIN; ZDB-GENE-030131-215; cf121.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR002108; Actbind cofin.
DR Pfam; PF00241; Cofilin_ADF; I.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Actbind_cofin; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
SQ SEQUENCE 165 AA; 18771 MW; 3FD3P8F542E2A707 CRC64;

Alignment Scores:
Pred. No.: 1.2e-45 Length: 165
Score: 625.50 Matches: 125
Percent Similarity: 85.03% Conservative: 17
Best Local Similarity: 74.85% Mismatches: 20
Query Match: 69.42% Indels: 5
DB: 2 Gaps: 2

US-10-649-952A-2 (1-501) x Q6TH32 (1-165)

QY 1 ATGGCGTCCGGTGGCTGCTCTCATGCTGTCATCAAGGTGTTCAAGCATGAGGTG 60
Db 1 MetAlaSerGlyValThrValGluGluThrValLeuPheAsnGluMetLysVal 20
QY 61 CGTAACTCTTCAACGCCAGAGAGAGGTGAAG---AAGCGCAAGAGCGGTCTCTCTGC 177
Db 21 ArgLysAlaHisCysAsnGluGluGluSerLysArgLysLysAlaValMetPheCys 40
QY 118 CTGAGTGGAGCAAGAAGAACATCATCTCTGGAGAGGGCAAGAGATCTCTGGTGGCGAT 177
Db 41 LeuSerAspLysLysHisIleMetGluGlnGlyGlnGluLeuGlnGlyAsp 60
QY 178 GTGGGCCAGACTGTGCGAGTCCCTACGCCACCTTCTCAAGTGTGCCAGATNAGGAC 237
Db 61 GluGly-----AspProTyrLeuLysPheValLysMetLeuProAsnAsp 76
QY 238 TGCCTGATGCCTCTATGATGCAACCTATGAGACCAAGAGAGCAAGAGAGGATCTG 297
Db 77 CysArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluThrLysLysGluAspLeu 96
QY 298 GTGTTTATCTTCTGGGCCCTCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCCAGC 357
Db 97 ValPheIlePheTyrAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSer 116
QY 358 TCCAGGAGCCCATCAAGAAGCTGACAGGATCAAGCATGATGATTCGAAGCAAACTGC 417
Db 117 SerLysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTyrGlnValAsnGly 136
QY 418 TAGCAGGAGGTCAAGAGCGCTGCACCTGCGAGAGAGTGGGGGCGAGTGGCGTCATC 477
Db 137 MetAspAlaIleLysAspArgLysThrLeuAlaGluLysLeuGlyGlyAlaSerValVal 156
QY 478 TCCCTGGAGGGCAAGCCTTTG 498
Db 157 SerLeuGluGlyLysProLeu 163

RESULT 15
DEST_CHICK STANDARD; PRT; 164 AA.
ID DEST_CHICK
AC P18359;
DT 01-NOV-1990 (Rel. 16, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Destrin (Actin-depolymerizing factor) (ADF).
GN Name:DSN; Synonyms:DSN;
OS Gallus gallus (Chicken).

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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 13, 2005, 09:48:26 ; Search time 30.5 Seconds
(without alignments)
2452.405 Million cell updates/sec

Title: US-10-649-952A-2
Perfect score: 901
Sequence: 1 atggctccggtgtggtgtg.....tggagggaagcctttgtga 501

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: ; 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q/cgn2_1/USPTO_spool_p/US10649952/runat_13052005_102650_27334/app_query.fasta_1.647
-DB=issued Patents AA -QFMT=fastan -SUFFIX=n2p.ral -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10649952 @CGN 1.1.46 @runat_13052005_102650_27334 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	628	69.7	127	4	US-09-513-999C-8059 Sequence 8059, Ap
2	606.5	67.3	165	4	US-09-513-999C-7957 Sequence 7957, Ap
3	354	39.3	86	4	US-09-513-999C-5489 Sequence 5489, Ap
4	287	31.9	69	4	US-09-513-999C-5488 Sequence 5488, Ap
5	242.5	26.9	146	4	US-09-513-999C-20627 Sequence 20627, A
6	188.5	20.9	154	4	US-09-723-830-2 Sequence 2, Appli
7	149	16.5	30	1	US-08-184-252A-5 Sequence 5, Appli
8	149	16.5	30	5	PCT-US95-00601-5 Sequence 5, Appli
9	124	13.8	28	4	US-09-017-689A-4 Sequence 4, Appli
10	124	13.8	30	1	US-08-184-252A-6 Sequence 6, Appli
11	124	13.8	30	5	PCT-US95-00601-6 Sequence 6, Appli
12	120	13.3	350	2	US-09-123-851-3 Sequence 3, Appli

13	120	13.3	350	2	US-08-728-520-3	Sequence 3, Appli
14	118	13.1	272	4	US-09-252-991A-31152	Sequence 31152, A
15	117.5	12.7	481	4	US-09-949-016-9748	Sequence 9748, Ap
16	116	12.9	350	1	US-08-184-252A-2	Sequence 2, Appli
17	116	12.9	350	5	PCT-US95-00601-2	Sequence 2, Appli
18	115	12.8	383	4	US-09-252-991A-20625	Sequence 20625, A
19	114.5	12.4	214	4	US-09-252-991A-19397	Sequence 19397, A
20	114	12.7	156	4	US-09-252-991A-31875	Sequence 31875, A
21	109.5	11.8	228	4	US-09-252-991A-28381	Sequence 28381, A
22	108	12.0	141	4	US-09-252-991A-28438	Sequence 28438, A
23	107	11.9	114	4	US-09-252-991A-31192	Sequence 31192, A
24	107	11.9	220	4	US-09-252-991A-17636	Sequence 17636, A
25	107	11.5	267	4	US-09-252-991A-28620	Sequence 28620, A
26	106.5	11.8	171	4	US-09-252-991A-26927	Sequence 26927, A
27	106.5	11.5	173	4	US-09-252-991A-32359	Sequence 32359, A
28	106	11.8	216	4	US-09-252-991A-32065	Sequence 32065, A
29	106	11.8	266	4	US-09-252-991A-19128	Sequence 19128, A
30	106	11.8	299	4	US-09-252-991A-17588	Sequence 17588, A
31	106	11.8	529	4	US-09-252-991A-26641	Sequence 26641, A
32	105.5	11.7	172	4	US-09-252-991A-17765	Sequence 17765, A
33	105.5	11.7	242	4	US-09-252-991A-27672	Sequence 27672, A
34	105.5	11.4	699	4	US-09-252-991A-26231	Sequence 26231, A
35	105	11.7	234	4	US-09-252-991A-28621	Sequence 28621, A
36	104.5	11.6	121	4	US-09-252-991A-26079	Sequence 26079, A
37	104.5	11.6	196	4	US-09-252-991A-16779	Sequence 16779, A
38	104.5	11.6	268	4	US-09-252-991A-17943	Sequence 17943, A
39	104	11.5	144	4	US-09-252-991A-24476	Sequence 24476, A
40	104	11.5	191	4	US-09-252-991A-23902	Sequence 23902, A
41	103.5	11.5	320	4	US-09-252-991A-24634	Sequence 24634, A
42	103.5	11.5	343	2	US-09-123-851-1	Sequence 1, Appli
43	103.5	11.5	343	2	US-08-728-520-1	Sequence 1, Appli
44	103	11.4	228	4	US-09-252-991A-18111	Sequence 18111, A
45	103	11.4	414	4	US-09-252-991A-31151	Sequence 31151, A

ALIGNMENTS

RESULT 1
US-09-513-999C-8059
; Sequence 8059, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8059
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 122
; OTHER INFORMATION: Xaa=Ala or Thr
US-09-513-999C-8059

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Pred. No.: 7.36e-62
Score: 628.00
Percent Similarity: 98.44%
Best Local Similarity: 98.44%
Query Match: 69.70%
Indels: 1
Gaps: 0
Length: 127
Matches: 126
Conservative: 0
Mismatch: 1

US-10-649-952A-2 (1-501) x US-09-513-999C-8059 (1-127)

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QY 61 CGTAAGTCTTCAACGCCAGAGAGGTGAAGAACGCGCAAGAGCGGTGCTCTTCTGCTG 120
Db 21 ArgLysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
QY 121 AGTGAGGACAGAGAACATCATCTCTGGAGAGGCGCAAGAGATCTGTGGGCGATGTG 180
Db 41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
QY 181 GGCACAGCTGCGACGATCCCTAGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
Db 61 GlyValThrIleThrAspProPheLysHisPheValGlyMetLeuProGluLysAspCys 80
QY 241 CGCTATGCTCTTATGATCAACCTATGACACCAAGAGAGAGCAAGAGGAGTCTGGTG 300
Db 81 ArgTyraLeuTyraAspAlaSerPheGluThrLysGluSerArgLysGluLeuMet 100
QY 301 TTTATCTTCTGGGCCCCGAGTCTGGCCCCCTTAAGAGCAAAATGATTATGCCAGTCC 360
Db 101 PheIlePheTrpAlaProGluLeuAlaProLeuLysSerLysMetIleTyraLeuSer 120
QY 361 AAGGAGCGCATCAAGAAGAAGC 382
Db 121 Lys-***ProSerArgArgSer 127
RESULT 2
US-09-513-999C-7957
; Sequence 7957, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 3681
; SOFTWARE: Patent.pm
; SEQ ID NO 7957
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-7957
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Score: 606.50 Matches: 118
Percent Similarity: 83.73% Conservative: 21
Best Local Similarity: 71.08% Mismatches: 26
Query Match: 67.31% Indels: 1
DB: 4 Gaps: 1
US-10-649-952A-2 (1-501) x US-09-513-999C-7957 (1-165)
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QY 121 AGTGAGGACAGAGAACATCATCTCTGGAGAGGCGCAAGAGATCTGTGGGCGATGTG 180
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QY 301 TTTATCTTCTGGGCCCCGAGTCTGGCCCCCTTAAGAGCAAAATGATTATGCCAGTCC 360
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QY 361 AAGGAGCGCATCAAGAAGAAGCTGACAGGATCAAGCATCAATTGCAAGCAAACTGCTAC 420
Db 121 LysAspAlaIleLysLysLysPheGlnGlyIleLysHisGluCysGlnAlaAsnGlyPro 140
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QY 481 CTGGAGGCGCAAGCCTTTG 498
Db 160 PheGluGlyCysProVal 165
RESULT 3
US-09-513-999C-5489
; Sequence 5489, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5489
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5489
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Pred. No.: 3.2e-31 Length: 86
Score: 354.00 Matches: 86
Percent Similarity: 89.53% Conservative: 10
Best Local Similarity: 77.91% Mismatches: 9
Query Match: 39.29% Indels: 0
DB: 4 Gaps: 0
US-10-649-952A-2 (1-501) x US-09-513-999C-5489 (1-86)
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QY 121 AGTGAGGACAGAGAACATCATCTCTGGAGAGGCGCAAGAGATCTGTGGGCGATGTG 180
Db 41 SerAspAspLysArgGlnIleIleValGluGluAlaLysGlnIleLeuValGlyAspIle 60
QY 181 GGCACAGCTGCGACGATCCCTAGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
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; ORGANISM: Candida albicans
US-09-248-796A-20627

Alignment Scores:
Pred. No.:      1.21e-18      Length:      146
Score:          242.50        Matches:     46
Percent Similarity: 59.57%    Conservative: 38
Best Local Similarity: 32.02% Mismatches:   36
Query Match:    26.91%       Indels:      21
DB:             4            Gaps:         3

US-10-649-952A-2 (1-501) x US-09-248-796A-20627 (1-146)

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Dd  26 -----LeuGlyArgLysTyrllysPheValIlePheThrLeuAsnAspGluLys 41
Qy  133 AAGAACATCATCCTCGAGAGGAGGCCAAGGAGATCTCTGTGGCGCATGTGGCCAGACTGTC 192
Dd  42 ThrGlnIleValValGluGln-----ThrserThr 51
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Qy  427 GTC 429
Dd  132 Val 132

RESULT 6
US-09-723-830-2
; Sequence 2, Application US/09723830
; Patent No. 6458930
; GENERAL INFORMATION:
; APPLICANT: Nislow, Corey
; APPLICANT: Wong, Kee
; TITLE OF INVENTION: Aspergillus fumigatus Cofilin
; FILE REFERENCE: 1039
; CURRENT APPLICATION NUMBER: US/09/723,830
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-723-830-2

Alignment Scores:
Pred. No.:      1.38e-12      Length:      154
Score:          188.50        Matches:     50
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Query Match:    20.92%       Indels:      25
DB:             4            Gaps:         7

US-10-649-952A-2 (1-501) x US-09-723-830-2 (1-154)
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Db 3 LeuAlaSerGlyValSerIleAlaAspGluCysIleThrAlaPheAsnAspPheArgMet 22
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QY 61 CGTAAGTCTTCAACGCCAGAGGAGGTGAAGAGCGGCGGTCTTCTGCTGCTG 120
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Db 23 SerGlyAsnLysAla-----AsnLysThrLysPheIleIlePheLysIle 37
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QY 121 AGTCAGACAAGAACAATCATCTCGAGAGGCGCAAGAGATCTGCTGGGCGATGTG 180
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Db 38 AlaAspAsnLysLysGluValValIleAspGlu-----Val 49
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QY 181 GGCCAGACTGTCGACGATCCTCCAGCCACCTTCTCAAGATGCTG---CCAGATAAGGAC 237
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Db 50 SerGln-----GluGluAspTyrGluValPheArgSerArgLeuGluAlaThrLysAsp 67
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QY 238 TGC-----CGTATGCCCTCTATGATGCAACCTATGAGACC----- 273
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Db 68 SerLysGlyAsnProAlaProArgTyrAlaValTyrAspValGluTyrAspLeuGlyGly 87
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QY 274 AAGGAGACGAAGAGGAGGATCGTGTCTTATCTTCTGCGCCCGGAGTCTGCGCCCTT 333
   :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 88 GlyGluGlyLysArgSerLysIleValPheIleSerTrpValProSerAspThrProThr 107
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QY 334 AAGAGCAAAATGATTTATGCCAGCTCCAAGGAGCCCATCAAGAGAAGCTGACAGGGATC 393
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Db 108 LeuTrpSerMetIleTyrAlaSerThrArgGluAsnLeuLysAsnAlaLeu---AsnIle 126
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QY 394 AAGCATGAATTCGAAGCAAACTGCTACGAGGAGGTCAAGGACCGCTGCACCTGCGCAGAG 453
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Db 127 HisThrSerIleHisAlaAspAspLysGlyAspIleGluTrpLysThrValLeuAlaGlu 146
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Db 147 AlaSerGlyGlyLysAla 152
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RESULT 7
US-08-184-252A-5
; Sequence 5, Application US/08184252A
; Patent No. 5573935
; GENERAL INFORMATION:
; APPLICANT: Beeler, John F.
; APPLICANT: LaRoche, William
; APPLICANT: Aaronson, Stuart A.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 18-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH084.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; PCT-US95-00601-5
Alignment Scores: 2.02e-08 Length: 30
Pred. No.: 149.00 Matches: 29
Score:
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-184-252A-5
Alignment Scores: 2.02e-08 Length: 30
Pred. No.: 149.00 Matches: 29
Score:
Percent Similarity: 96.67%
Best Local Similarity: 96.67%
Query Match: 16.54%
Indels: 0
Gaps: 1
DB:
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QY 361 AAGGAGCCCATCAAGAGAAGAGCTGACAGGG 390
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RESULT 8
PCT-US95-00601-5
; Sequence 5, Application PC/TUS9500601
; GENERAL INFORMATION:
; APPLICANT: United States of America Department of Health and Human
; APPLICANT: Services
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH084.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; PCT-US95-00601-5
Alignment Scores: 2.02e-08 Length: 30
Pred. No.: 149.00 Matches: 29
Score:
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Percent Similarity: 96.67% Conservative: 0
Best Local Similarity: 96.67% Mismatches: 1
Query Match: 16.54% Indels: 0
DB: 5 Gaps: 0

US-10-649-952A-2 (1-501) x PCT-US95-00601-5 (1-30)

QY 301 TTTATCTTCTGGCCCGAGTCTGGCCCTTAAGAGCAAAATGATTATGCCAGTCC 360
Db 1 PheilePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyAlaSer 20
QY 361 AAGAGCCCATCAAGAAGAGCTGACAGGG 390
Db 21 LysAspAlaIleLysLysPheThrGly 30

RESULT 9

US-09-017-689A-4
; Sequence 4, Application US/09017689A
; Patent No. 6413940
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, Paul
; TITLE OF INVENTION: PHARMACEUTICALLY ACTIVE AGENTS THAT
; IMPEDE THE FORMATION OF AMYLOID BY IMPEDING THE GENESIS OF
; DMS

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,689A
FILING DATE: 03-Feb-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/038,694
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 018792/0125
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-017-689A-4

Alignment Scores:
Pred. No.: 1,25e-05 Length: 28
Score: 124.00 Matches: 24
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 0
Query Match: 13.76% Indels: 0
DB: 4 Gaps: 0

US-10-649-952A-2 (1-501) x US-09-017-689A-4 (1-28)

QY 136 AACATCATCTGAGAGGAGGAGATCCTGGTGGCGATGTGGCCAGACTGTGCGAC 195
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Db 1 AsnIleIleLeuGluGluGlyLysAspIleLeuValGlyGlnThrValasp 20
QY 196 GATCCCTACGCCACC 210
|||||
Db 21 AspProTyAlaThr 25

RESULT 10

US-08-184-252A-6
; Sequence 6, Application US/08184252A
; Patent No. 5573935
; GENERAL INFORMATION:
; APPLICANT: Beeler, John F.
; APPLICANT: Larochele, William
; APPLICANT: Aaronson, Stuart A.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,252A
FILING DATE: 18-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned A.

REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH084.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

US-08-184-252A-6

Alignment Scores:
Pred. No.: 1,28e-05 Length: 30
Score: 124.00 Matches: 22
Percent Similarity: 90.00% Conservative: 5
Best Local Similarity: 73.33% Mismatches: 3
Query Match: 13.76% Indels: 0
DB: 1 Gaps: 0

US-10-649-952A-2 (1-501) x US-08-184-252A-6 (1-30)

QY 301 TTTATCTTCTGGCCCGAGTCTGGCCCTTAAGAGCAAAATGATTATGCCAGTCC 360
Db 1 PheileLeuTrpAlaProAspSerAlaProIleLysSerLysMetTyrThrSerThr 20
QY 361 AAGAGCCCATCAAGAAGAGCTGACAGGG 390
|||||
Db 21 LysAspSerIleLysLysLeuValGly 30

RESULT 11

PCT-US95-00601-6
; Sequence 6, Application PCT/TUS9500601
; GENERAL INFORMATION:

APPLICANT: United States of America Department of Health and Human
APPLICANT: Services
TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobel, Martens Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00601
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH084.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
PCT-US95-00601-6

Alignment Scores:
Pred. No.: 1.29e-05 Length: 30
Score: 124.00 Matches: 22
Percent Similarity: 90.00% Conservative: 5
Best Local Similarity: 73.33% Mismatches: 3
Query Match: 13.76% Indels: 0
DB: 5 Gaps: 0

US-10-649-952A-2 (1-501) x PCT-US95-00601-6 (1-30)

Qy 301 TTTATCTTCTGGCCCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCCAGCTCC 360
Db 1 PheileuTrpAlaProAspSerAlaProIleLysSerLysMetMetTyrThrSerThr 20

Qy 361 AAGCAGCCATCAAGAAGAGCTGACAGG 390
Db 21 LysaspSerIleLysLysLysLysValGly 30

RESULT 12
US-09-123-851-3
Sequence 3, Application US/09123851
Patent No. 5958405
GENERAL INFORMATION:
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,851
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/728,520
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0136 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 451482
US-09-123-851-3

Alignment Scores:
Pred. No.: 8.83e-05 Length: 350
Score: 120.00 Matches: 34
Percent Similarity: 55.56% Conservative: 36
Best Local Similarity: 26.98% Mismatches: 40
Query Match: 13.32% Indels: 16
DB: 2 Gaps: 6

US-10-649-952A-2 (1-501) x US-09-123-851-3 (1-350)

Qy 79 GAGGAGGTGAAGAAGCGCAAGAGGGGTCTTCTGCTGAGTGGAGCAAGAAGAAC 138
Db 11 GluAspValLysGlu-----IlePheAlaArgAlaArgAsnGlyLysTyr 25

Qy 139 ATCATCTCTGAG-----GAGGCAAGAGATCTGCTGGCGCATGTGGGCCAG-- 186
Db 26 ArgLeuLeuLysIleSerIleGluAsnGluGlnLeuValIleGlySerTyrSerGlnPro 45

Qy 187 -----ACTGTCGACGATCCCTACGCCACCTTTTGTCTC---AAGATGCTGCCAGATAAGGAC 237
Db 46 SerAspSerTrpAspLysAspTyrAspSerPheValLeuProLeuLeuGluAspLysGln 65

Qy 238 TGGCGGTATCCCTCTATGATGCAACTATGACCAAGAGAGAGCAAGAGAGGATCTG 297
Db 66 ProCysTyrIleLeuPhe-----ArgLeuAspSerGlnAsnAlaGlnGlyTyrGluTrp 83

Qy 298 GTGTTTATCTTCTGGGCCCCCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCCAGC 357
Db 84 IlePheIleAlaTrpSerProAspHisSerHisValArgGlnLysMetLeuTyrAlaAla 103

Qy 358 TCCAAGGACGCCCATCAAGAAGAAGCTGACACG-----ATCAGCATGAATTCACAGCA 411
Db 104 ThrArgAlaThrLeuLysLysGluPheGlyGlyHisIleLysAspGluValPheGly 123

Qy 412 AACTGCTACGAGGATC 429
Db 124 ThrValLysGluAspVal 129

RESULT 13
US-08-728-520-3
Sequence 3, Application US/08728520
Patent No. 5994112
GENERAL INFORMATION:
APPLICANT: Goli, Surya K.


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Db 188 -----AlaTrpAlaTrpLysArgSerArgLeuPheSerSerMetAlaArgAla 204
QY 455 -----AGCTGGGGGGCAGTGGGTCA--TCTCCTCGAGGCA-----AGCCTTGT 499
Db 205 GlyAspSerSerGlyAlaCysArgSerArgSerSerTrpArgSerCysArgSerIleCys 224

RESULT 15
US-09-949-016-9748
; Sequence 9748, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9748
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9748
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Alignment Scores:
Pred. No.: 0.000189 Length: 481
Score: 117.50 Matches: 48
Percent Similarity: 31.58% Conservative: 6
Best Local Similarity: 28.07% Mismatches: 50
Query Match: 12.68% Indels: 67
DB: 4 Gaps: 9
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US-10-649-952A-2 (1-501) x US-09-949-016-9748 (1-481)

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QY 490 TGCCTCCAGGAGATGACCGCACTGCCCGCCAGCTTCTGTCCAGGGTGCAGCGTCTCT 431
Db 277 CysThrThrArgArgLeuProGlnProProProProProProProProProProPro 292
QY 430 TGACCTCCTCGTAGAGTTGCTTGCATTCGCAATTCATGCTTGATCCCTGTGAGTCTTCTTGA 371
Db 293 ProProProSerSer----- 297
QY 370 TGGCGTCTCTGGAGCTGCATAAATCATTTTGCTCTTAAGGGCGCAGACTCGGGGGGCC 311
Db 298 -----GlnAlaArgCysPro 302
QY 310 AGAAGATAAACACAGATCCTCTTCTGTCTCTCT----- 275
Db 303 ProArg-----AlaProProThrArgAlaProSerMetGlnAlaThrArgArgArg 319
QY 274 ---TGGTCTCATAGTTGCATCATAGAGGGCATAGCGGCAGTCTCTTATCTGGCAGCATCT 218
Db 320 ArgTrpProArgArgLeuGlnSerThrThrProArgArgArgProAlaLeuAlaAlaSer 339
QY 217 TGACAAAGTGG-----CGTAGGATCGTCGACAGTCTGCCCATCCATCCG----- 173
Db 340 ---SerAlaTrpPheLeuSerGlyArgSerAlaGlnSerTrpGlyProHisArgArgGly 358
QY 172 -----CCACGAGATCTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 137
Db 359 ProAlaAlaLeuAlaProLeuProProProProProProProProProProProProPro 378
QY 136 ---TCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 80
Db 379 ProGlnAlaAlaProGlyProGlyArgProThrPro-----ProPro 392
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QY 79 CTGGCGTTGAAGACTTACGCACCTTTCATGTCTGT 47
Db 393 MetArgLeuProThrArgAlaProThrAlaArg 403
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Search completed: May 13, 2005, 10:01:42
Job time : 32.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 13, 2005, 09:50:51 ; Search time 106.5 Seconds
(without alignments)
3142.909 Million cell updates/sec

Title: US-10-649-952A-2
Perfect score: 901
Sequence: 1 atggctccgggtgctgtgctgt.....tggagggaagcctttgtga 501

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 2864370

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications AA -QWMT=fastan -SUFFIX=n2p.rapb -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10649952 @CGN 1 1 199 @runat 13052005_27349
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA:*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No. Score Match Length DB ID Description

No.	Score	Match	Length	DB	ID	Description
1	846	93.9	166	16	US-10-649-952A-1	Sequence 1, Appl
2	764	84.8	149	16	US-10-408-765A-2270	Sequence 2270, Ap
3	702	77.9	166	14	US-10-205-342-21	Sequence 21, Appl
4	699	77.6	166	14	US-10-208-823-72	Sequence 72, Appl
5	699	77.6	166	16	US-10-408-765A-1910	Sequence 1910, Ap
6	699	77.6	205	15	US-10-158-034-93	Sequence 93, Appl
7	557.5	61.9	148	16	US-10-408-765A-2351	Sequence 2351, Ap
8	460	51.1	129	15	US-10-158-034-94	Sequence 94, Appl
9	450	49.9	156	15	US-10-158-034-68	Sequence 68, Appl
10	273	30.3	106	15	US-10-264-049-4340	Sequence 4340, Ap
11	267.5	29.7	143	15	US-10-369-493-22293	Sequence 22293, A
12	253.5	28.1	141	16	US-10-263-255-2	Sequence 2, Appl
13	245.5	27.2	141	16	US-10-263-255-4	Sequence 4, Appl
14	239.5	26.6	139	15	US-10-424-599-186070	Sequence 186070, A
15	230	25.5	60	14	US-10-029-386-30107	Sequence 30107, A
16	230	25.5	190	15	US-10-369-493-2272	Sequence 2272, Ap
17	227	25.2	145	15	US-10-425-114-37040	Sequence 37040, A
18	227	25.2	161	15	US-10-425-114-59591	Sequence 59591, A
19	227	25.2	171	15	US-10-425-114-39098	Sequence 39098, A
20	227	25.2	179	15	US-10-425-114-38879	Sequence 38879, A
21	227	25.2	179	15	US-10-425-114-41223	Sequence 41223, A
22	227	25.2	179	15	US-10-425-114-44883	Sequence 44883, A
23	227	25.2	179	15	US-10-425-114-51312	Sequence 51312, A
24	227	25.2	179	15	US-10-425-114-57582	Sequence 57582, A
25	227	25.2	179	15	US-10-425-114-59194	Sequence 59194, A
26	227	25.2	179	15	US-10-425-114-59883	Sequence 59883, A
27	227	25.2	179	15	US-10-425-114-66714	Sequence 66714, A
28	227	25.2	179	15	US-10-425-114-67765	Sequence 67765, A
29	227	25.2	179	15	US-10-425-114-72052	Sequence 72052, A
30	227	25.2	179	15	US-10-425-114-72097	Sequence 72097, A
31	224.5	24.9	139	16	US-10-767-701-45854	Sequence 45854, A
32	223.5	24.8	194	16	US-10-767-701-43979	Sequence 43979, A
33	221	24.5	139	15	US-10-250-613-9	Sequence 9, Appl
34	221	24.5	157	15	US-10-425-114-59062	Sequence 59062, A
35	221	24.5	173	15	US-10-425-114-66010	Sequence 66010, A
36	221	24.5	176	15	US-10-425-114-69864	Sequence 69864, A
37	221	24.5	177	15	US-10-425-114-44953	Sequence 44953, A
38	221	24.5	177	15	US-10-425-114-48026	Sequence 48026, A
39	221	24.5	177	15	US-10-425-114-48329	Sequence 48329, A
40	221	24.5	177	15	US-10-425-114-49519	Sequence 49519, A
41	221	24.5	177	15	US-10-425-114-53265	Sequence 53265, A
42	221	24.5	177	15	US-10-425-114-53325	Sequence 53325, A
43	221	24.5	177	15	US-10-425-114-66577	Sequence 66577, A
44	221	24.5	177	15	US-10-425-114-66602	Sequence 66602, A
45	221	24.5	181	15	US-10-425-114-69951	Sequence 69951, A

ALIGNMENTS

RESULT 1

US-10-649-952A-1
; Sequence 1, Application US/10649952A
; Publication No. US20040157326A1
; GENERAL INFORMATION:
; APPLICANT: DAIICHI SUNTORY PHARMA CO., LTD.
; APPLICANT: DAIICHI SUNTORY PHARMA CO., LTD.
; APPLICANT: Miura, Kenju
; APPLICANT: Haruyama, Munetada
; APPLICANT: Kodama, Shio
; TITLE OF INVENTION: Promoters of the growth and/or differentiation of hematopoietic stem cells and/or hematopoietic progenitors
; FILE OF INVENTION: stem cells and/or hematopoietic progenitors
; FILE REFERENCE: 58777.000013
; CURRENT APPLICATION NUMBER: US/10/649,952A
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: PCT/JP02/13862
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: JAPAN 400330/2001
; PRIOR FILING DATE: 2001-12-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1

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; LENGTH: 166
; TYPE: PRT
; ORGANISM: Human
US-10-649-952A-1
Alignment Scores:
Pred. No.: 1.09e-73 Length: 166
Score: 846.00 Matches: 166
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.90% Indels: 0
DB: 16 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-649-952A-1 (1-166)
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DB 1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20
QY 61 CGTAAGTCTTCAACGCCAGAGGAGGTGAAGAGCGCAAGAGCGGTGCTCTTCTGCGCTG 120
DB 21 ArgLysSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
QY 121 AGTGAGGACAAAGAAACATCATCTCGAGGAGGCGCAAGGAGATCCCTGGTGGCGATGTG 180
DB 41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
QY 181 GGCAGACTGTCGACGATCCCTACGCCACCTTTGTCAAGATGTCGCCAGATAAGGACTGC 240
DB 61 GlyInThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCys 80
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DB 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
QY 301 TTTATCTTCTGGGCCCGCGAGTCTGCGCCCTTAAGAGCAAAATGATTATTCGCGAGTCC 360
DB 101 PheIlePheTyrAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSer 120
QY 361 AAGAGCGCATCAAGAGAGCTGACAGGGATCAAGCATGAATTCGAAGCAAACTGCTAC 420
DB 121 LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyr 140
QY 421 GAGGAGTCAAGGACCCCTGACCCCTGCGAGAGAGCTGGGGGCGAGTGGGTCATCTCC 480
DB 141 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer 160
QY 481 CTGAGGGCGCAAGCCTTTG 498
DB 161 LeuGluGlyLysProLeu 166

RESULT 2
US-10-408-765A-2270
; Sequence 2270, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2270
; LENGTH: 149
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-408-765A-2270
Alignment Scores:
Pred. No.: 1.06e-65 Length: 149
Score: 764.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.79% Indels: 0
DB: 16 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-408-765A-2270 (1-149)
QY 52 ATGAAGTGGTAAAGTCTTCAACGCCAGAGGAGGTGAAGAGCGCAAGAGCGGTGCTC 111
DB 1 MetLysValArgLysSerThrProGluGluValLysLysArgLysLysAlaValLeu 20
QY 112 TTCTGCCCTGAGTGAGGACAAAGAACATCATCTCTGGAGGAGGCGCAAGGAGATCCTGGTG 171
DB 21 PheCysLeuSerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuVal 40
QY 172 GGCAGTGTGGCCAGACTGTGCGAGCATCCCTACGCCACCTTTGTCAAGATGCTGCCAGAT 231
DB 41 GlyAspValGlyInThrValAspAspProTyrAlaThrPheValLysMetLeuProAsp 60
QY 232 AAGGACTGCCGCTATGCTCTATGATGCAACCTATGAGACCAAGGAGGAGCAAGAGGAG 291
DB 61 LysAspCysArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGlu 80
QY 292 GATCTGTGTATTCTTCTGGGCCCGCGAGTCTGCGCCCTTAAGAGCAAAATGATTAT 351
DB 81 AspleuValPheIlePheTyrAlaProGluSerAlaProLeuLysSerLysMetIleTyr 100
QY 352 GCAGCTCCAAGAGCGCATCAAGAGAGCTGACAGGATCAAGCATGAATTCGAAGCA 411
DB 101 AlaSerSerLysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAla 120
QY 412 AACTGTCTACGAGGAGGTCAAGGACCGCTGCACCTGCGAGAGAGCTGGGGGCGAGTGC 471
DB 121 AsnCysTyrGluGluValLysAspArgCysThrLeuAlaGluLysLeuGlySerAla 140
QY 472 GTCATCTCCCTGGAGGCGCAAGCCTTTG 498
DB 141 ValIleSerLeuGluGlyLysProLeu 149

RESULT 3
US-10-205-342-21
; Sequence 21, Application US/10205342
; Publication No. US20030108906A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WI-A-018198
; CURRENT APPLICATION NUMBER: US/10/205,342
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Protein: Cofilin
US-10-205-342-21
Alignment Scores:
Pred. No.: 1.21e-59 Length: 166
```

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Score: 702.00 Matches: 135
Percent Similarity: 89.76% Conservative: 14
Best Local Similarity: 81.33% Mismatches: 17
Query Match: 77.91% Indels: 0
DB: 14 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-205-342-21 (1-166)

QY 1 ATGGCTCCGGTGTGCTCTGATGTTTCATCAAGGTGTTCAACGACATCAAGGTG 60
DB 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20
QY 61 CGTAAGTCTTCAAGCCAGAGGAGTCAAGAGCGCAAGAGCGGTCTTCTGCGCTG 120
DB 21 ArgLysSerSerThrGlnGluGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40
QY 121 AGTGAGGACAAAGAACATCATCTCGAGAGGGCAAGAGATCCTGTGGGCGATGTG 180
DB 41 SerAspAspLysArgGlnIleValGluGluAlaLysGlnIleLeuValGlyAspIle 60
QY 181 GGCAGACTCTGACGATCCCTAGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
DB 61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 80
QY 241 CGTATGCTCTATGATGCAACCTATGACAGGATCAAGCATGAATTTGCAAGCAAACTGCTGC 300
DB 81 ArgTyraLeuLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
QY 301 TTTATCTTCTGGCCCGGAGTCTGCCACCTTTAAGAGCAAAATGATTTATGCGAGTCC 360
DB 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
QY 361 AAGGAGCCATCAAGAGAGCTGACAGGATCAAGCATGAATTTGCAAGCAAACTGCTGC 420
DB 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 140
QY 421 GAGGAGTCAAGAGCCGCTGACCCCTGGCAGAGAACTGGGGGCGAGTGGCGTCACTCC 480
DB 141 AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyGlySerValValSer 160
QY 481 CTGAGGGCAAGCCTTTG 498
DB 161 LeuGluGlyLysProLeu 166

RESULT 4
US-10-649-952A-2 (1-501) x US-10-205-342-21 (1-166)
; Sequence 72, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746

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; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-72

Alignment Scores:
Pred. No.: 2,37e-59 Length: 166
Score: 699.00 Matches: 134
Percent Similarity: 89.76% Conservative: 15
Best Local Similarity: 80.72% Mismatches: 17
Query Match: 77.58% Indels: 0
DB: 14 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-205-823-72 (1-166)

QY 1 ATGGCTCCGGTGTGCTCTGATGTTTCATCAAGGTGTTCAACGACATCAAGGTG 60
DB 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20
QY 61 CGTAAGTCTTCAAGCCAGAGGAGTCAAGAGCGCAAGAGCGGTCTTCTGCGCTG 120
DB 21 ArgLysSerSerThrGlnGluGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40
QY 121 AGTGAGGACAAAGAACATCATCTCGAGAGGGCAAGAGATCCTGTGGGCGATGTG 180
DB 41 SerAspAspLysArgGlnIleValGluGluAlaLysGlnIleLeuValGlyAspIle 60
QY 181 GGCAGACTCTGACGATCCCTAGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
DB 61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 80
QY 241 CGTATGCTCTATGATGCAACCTATGACAGGATCAAGCATGAATTTGCAAGCAAACTGCTGC 300
DB 81 ArgTyraLeuLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
QY 301 TTTATCTTCTGGCCCGGAGTCTGCCACCTTTAAGAGCAAAATGATTTATGCGAGTCC 360
DB 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
QY 361 AAGGAGCCATCAAGAGAGCTGACAGGATCAAGCATGAATTTGCAAGCAAACTGCTGC 420
DB 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 140
QY 421 GAGGAGTCAAGAGCCGCTGACCCCTGGCAGAGAACTGGGGGCGAGTGGCGTCACTCC 480
DB 141 AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyGlySerValValSer 160
QY 481 CTGAGGGCAAGCCTTTG 498
DB 161 LeuGluGlyLysProLeu 166

RESULT 5
US-10-408-765A-1910
; Sequence 1910, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boim D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A

```

; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1910
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1910

Alignment Scores:
Pred. No.: 2,37e-59 Length: 166
Score: 699.00 Matches: 134
Percent Similarity: 89.76% Conservative: 15
Best Local Similarity: 80.72% Mismatches: 17
Query Match: 77.58% Indels: 0
DB: 16 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-408-765A-1910 (1-166)

```
QY 1 ATGGCTCCGGTGGCTGCTCTCTGATGGTGTCTCATCAAGGTGTTCAACGACATCAAGGTG 60
    |||...|||
Db 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetCysVal 20

QY 61 CGTAAGTCTTCAACGCCAGGAGGTGAAGAAGCGCAAGAGCGGCTCTTCTGCTG 120
    |||...|||
Db 21 ArgLysSerSerThrGlnGluGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40

QY 121 AGTGAGCAACAAGAACATCATCTCTGGAGGAGGCAAGGATCCTGGTGGCGATGTG 180
    |||...|||
Db 41 SerAspAspLysArgGlnIleValGluGluAlaLysGlnIleLeuValGlyAspIle 60

QY 181 GGCCAGACTGTCGACGATCCCTACGCCACCTTTCTCAAGATGCTGCCAGATAAGGACTGC 240
    |||...|||
Db 61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuProLeuAsnAspCys 80

QY 241 CGCTATGCCCTCTATGATGCAACCTATGACACCAAGGAGGCAAGAAGGAGGATCTGGTG 300
    |||...|||
Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100

QY 301 TTTATCTTGGGCCCCGAGTCTGGCCCCCTTAAAGAGCAAAATGATTATGCCAGCTCC 360
    |||...|||
Db 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120

QY 361 AAGCAGCCATCAAGAAGAGCTCACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
    |||...|||
Db 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 140

QY 421 GAGGAGTCAAGGACCGCTGCACCTCGCAGAGAGCTGGGGGCGAGTGGCGGTCTCATCTCC 480
    |||...|||
Db 141 AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyGlyAsnValValSer 160

QY 481 CTGAGGAGCAAGCCTTTG 498
    |||...|||
Db 161 LeuGluGlyLysProLeu 166
```

RESULT 6

US-10-158-034-93
; Sequence 93, Application US/10158034
; Publication No. US20030219758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PZ10C1
; CURRENT APPLICATION NUMBER: US/10/158,034
; CURRENT FILING DATE: 2002-05-31
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-034-93

Alignment Scores:

Pred. No.: 2,49e-59 Length: 205
Score: 699.00 Matches: 134
Percent Similarity: 89.76% Conservative: 15
Best Local Similarity: 80.72% Mismatches: 17
Query Match: 77.58% Indels: 0
DB: 15 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-158-034-93 (1-205)

```
QY 1 ATGGCTCCGGTGGCTGCTCTCTGATGGTGTCTCATCAAGGTGTTCAACGACATCAAGGTG 60
    |||...|||
Db 40 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetCysVal 59

QY 61 CGTAAGTCTTCAACGCCAGGAGGTGAAGAAGCGCAAGAGCGGCTCTTCTGCTG 120
    |||...|||
Db 60 ArgLysSerSerThrGlnGluGluIleLysLysArgLysLysAlaValLeuPheCysLeu 79

QY 121 AGTGAGCAACAAGAACATCATCTCTGGAGGAGGCAAGGATCCTGGTGGCGATGTG 180
    |||...|||
Db 80 SerAspAspLysArgGlnIleValGluGluAlaLysGlnIleLeuValGlyAspIle 99

QY 181 GGCCAGACTGTCGACGATCCCTACGCCACCTTTCTCAAGATGCTGCCAGATAAGGACTGC 240
    |||...|||
Db 100 GlyAspThrValGluAspProTyrThrSerPheValLysLeuProLeuAsnAspCys 119

QY 241 CGCTATGCCCTCTATGATGCAACCTATGACACCAAGGAGGCAAGAAGGAGGATCTGGTG 300
    |||...|||
Db 120 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 139

QY 301 TTTATCTTGGGCCCCGAGTCTGGCCCCCTTAAAGAGCAAAATGATTATGCCAGCTCC 360
    |||...|||
Db 140 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 159

QY 361 AAGCAGCCATCAAGAAGAGCTCACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
    |||...|||
Db 160 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 179

QY 421 GAGGAGTCAAGGACCGCTGCACCTCGCAGAGAGCTGGGGGCGAGTGGCGGTCTCATCTCC 480
    |||...|||
Db 180 AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyGlyAsnValValSer 199

QY 481 CTGAGGAGCAAGCCTTTG 498
    |||...|||
Db 200 LeuGluGlyLysProLeu 205
```

RESULT 7

US-10-408-765A-2351
; Sequence 2351, Application US/10408765A
; Publication No. US2004010187A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2351
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2351

Alignment Scores:

Pred. No.: 1,45e-45 Length: 148
Score: 557.50 Matches: 108
Percent Similarity: 84.56% Conservative: 18
Best Local Similarity: 72.48% Mismatches: 22
Query Match: 61.88% Indels: 1
DB: 16 Gaps: 1

US-10-649-952A-2 (1-501) x US-10-408-765A-2351 (1-148)

QY 52 ATGAAGTGGTGAAGTCTTCAACGCCAGAGAGGTGAAGAGCGCGGTGCTC 111
Db 1 MetLysValArgLysCysSerThrProGluIleLysLysArgLysLysAlaValIle 20
QY 112 TTCTGCTGAGTGAAGCAAGACATCATCTGGAGAGGCGAAGAGATCCTGGTG 171
Db 21 PheCysLeuSerAlaAspLysLysCysIleValGluGluGlyLysGluIleLeuVal 40
QY 172 GCGGATGTGGCCAGACTGCGAGCATCTCCAGCCACCTTCTCAAGATGCTGCCAGAT 231
Db 41 GlyAspValGlyValThrIleThrAspPropheLysHisPheValGlyMetLeuProGlu 60
QY 232 AAGGACTCGCGCTATGCTCTATGATCAACCTATGAGACCAAGAGAGCAAGAGAGGAG 291
Db 61 LysAspCysArgTyrAlaLeuTyrAspAlaSerPheGluThrLysGluSerArgLysGlu 80
QY 292 GATCTGTGTTATCTTCTGGGCCCGAGTCTGCGCCCTTAAAGAGCAAAATGATTAT 351
Db 81 GluLeuMetPhePheLeuTyrAlaProGluLeuAlaProLeuLysSerLysMetIleTyr 100
QY 352 GCAGCTCCAGAGACGCCATCAAGAGAGCTGACAGGATCAAGATGATGCAAGCA 411
Db 101 AlaSerSerLysAspAlaIleLysLysLysPheGlnGlyIleLysHisGluCysGlnAla 120
QY 412 AACTGTACAGAGAGGTCAAGGACCGCTGCACCTGCGAGAGAGCTGGGGGCGAGTGGC 471
Db 121 AsnGlyProGluAspLeuAsnArgAlaCys---IleAlaGluLysLeuGlySerLeu 139
QY 472 GTCATCTCCCTGGAGGCAAGCCTTTG 498
Db 140 IleValAlaPheGluGlyCysProVal 148

RESULT 8

US-10-158-034-94
; Sequence 94, Application US/10158034
; Publication No. US20030219758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ10C1
; CURRENT APPLICATION NUMBER: US/10/158,034
; CURRENT FILING DATE: 2002-05-31
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (107)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (126)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (127)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (128)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-158-034-94

Alignment Scores:

Pred. No.: 4,53e-36 Length: 129
Score: 460.00 Matches: 87
Percent Similarity: 90.65% Conservative: 10
Best Local Similarity: 81.31% Mismatches: 10
Query Match: 51.05% Indels: 0
DB: 15 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-158-034-94 (1-129)

QY 1 ATGGCTCCCGGTGCTGCTCTCTGATGTCATCAAGGTGTTCAACGACATGAAGGTG 60
Db 13 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 32
QY 61 CGTAAGTCTTCAACGCCAGAGAGGTGAAGAGCGCAAGAGCGGTGCTCTTCTCCCTG 120
Db 33 ArgLysSerSerThrGlnGluIleLysLysArgLysLysAlaValLeuPheCysLeu 52
QY 121 AGTGAGGCAAGAGCAATCATCTCTGGAGAGGCGAAGAGATCTCTGTGGCGATGTG 180
Db 53 SerAspAspLysArgGlnIleValGluGluAlaLysGlnIleLeuValGlyAspIle 72
QY 181 GCCAGACTGTCGAGATCCCTACGCCCTTGTCAAGATCTGCCAGATGAAGGACTGC 240
Db 73 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 92
QY 241 CGCTATGCCCTCTATGATCAACCTATGAGACCAAGAGAGCAAGAGAGATCTGGTG 300
Db 93 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSer***LysGluAspLeuVal 112
QY 301 TTTATCTTCTGGCCCCCGAG 321
Db 113 PheIlePheTrpAlaProGlu 119

RESULT 9

US-10-158-034-68
; Sequence 68, Application US/10158034
; Publication No. US20030219758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ10C1
; CURRENT APPLICATION NUMBER: US/10/158,034
; CURRENT FILING DATE: 2002-05-31
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-158-034-68
Alignment Scores:
Pred. No.: 4,48e-35 Length: 156
Score: 450.00 Matches: 85
Percent Similarity: 91.35% Conservative: 10
Best Local Similarity: 81.73% Mismatches: 9
Query Match: 49.94% Indels: 0
DB: 15 Gaps: 0
US-10-649-952A-2 (1-501) x US-10-158-034-68 (1-156)
QY 1 ATGGCTCCCGGTGCTGCTCTCTGATGTCATCAAGGTGTTCAACGACATGAAGGTG 60
Db 45 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 64

QY 61 CGTAAGTCTTCAACGCCAGAGGAGTGAAGAGCGCAAGAGCGGTCTTCTGCTG 120
 |||||
 Db 65 ArglySerSerThrGlnGluLeuIleLysLysLysLysLysLysLysLysLysLys 84
 |||||
 QY 121 AGTGAGGACAAAGAACATCATCTCGAGAGGCGCAAGAGATCTCTGGTGGCGATGTG 180
 |||||
 Db 85 SerAspLysArgGlnIleValGluLysGlnIleLysGlnIleLysValGlyAspIle 104
 |||||
 QY 181 GGCAGAGTCTGACAGATCCCTAGCCACCTTCTCAAGATGCTGCCAGATAAGGACTGC 240
 |||||
 Db 105 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 124
 |||||
 QY 241 CGCTATGCGCTCTATGATCAACCTATGAGACCAAGAGAGCAAGAGGAGATCTGGTG 300
 |||||
 Db 125 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 144
 |||||
 QY 301 TTTATCTCTGG 312
 |||||
 Db 145 PheIlePheTrp 148

RESULT 10

US-10-264-049-4340
 ; Sequence 4340, Application US/10264049
 ; Publication No. US20040005579A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P4133P1
 ; CURRENT APPLICATION NUMBER: US/10/264,049
 ; CURRENT FILING DATE: 2002-10-04
 ; PRIOR APPLICATION NUMBER: PCT/US01/18569
 ; PRIOR FILING DATE: 2001-06-07
 ; PRIOR APPLICATION NUMBER: US 60/209,467
 ; PRIOR FILING DATE: 2000-06-07
 ; NUMBER OF SEQ ID NOS: 4360
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO 4340
 ; LENGTH: 106
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (91)-
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (100)
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 US-10-264-049-4340

Alignment Scores:
 Pred. No.: 7,46e-18 Length: 106
 Score: 273.00 Matches: 58
 Percent Similarity: 67.62% Conservative: 13
 Best Local Similarity: 55.24% Mismatches: 34
 Query Match: 30.30% Indels: 0
 DB: 15 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-264-049-4340 (1-106)

QY 22 TCTGATGGTGCATCAAGGTGTTCAACGACATGAAGTGGCTAAGTCTTCAACGCCAGAG 81
 |||||
 Db 1 AlaAspGluValCysArgIlePheTyrAspMetLysValArgLysCysSerThrProGlu 20
 |||||
 QY 82 GAGGTGAAGAGCGCAAGAGCGGTGCTCTTCTGCTGAGTGAGGACAAAGAACATC 141
 |||||
 Db 21 GluIleLysLysArgLysLysAlaValIlePheCysLeuSerAlaAspLysLysCysIle 40
 |||||
 QY 142 ATCTGAGGAGGCGCAGGAGATCTGTGGGCGATGTGGGCGAGCTGCGAGATCCC 201
 |||||
 Db 41 IleValGluGluGlyLysGluIleLeuValGlyAspValGlyValThrIleThrAspPro 60

QY 202 TAGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGCGCGTATGCCTTATGATGCA 261
 |||||
 Db 61 PheIleHisPheValGlyMetLeuLeuLysLysIleValAlaMetLeuCysMetMetGln 80
 |||||
 QY 262 ACCTATGAGACCAAGGAGAGCAAGAGGAGATCTGTGTTTATCTTCTGGGCCCCGAG 321
 |||||
 Db 81 AlaLeuLysGlnLysAsnSerGluLysLys***LeuMetPhePheTrpGlyAlaPro*** 100
 |||||
 QY 322 TCTGCGCCCTTAAG 336
 |||||
 Db 101 LeuGlyThrPheLys 105

RESULT 11

US-10-369-493-22293
 ; Sequence 22293, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 22293
 ; LENGTH: 143
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 US-10-369-493-22293

Alignment Scores:
 Pred. No.: 2,76e-17 Length: 143
 Score: 267.50 Matches: 54
 Percent Similarity: 59.44% Conservative: 31
 Best Local Similarity: 29.76% Mismatches: 37
 Query Match: 27.69% Indels: 21
 DB: 15 Gaps: 3

US-10-649-952A-2 (1-501) x US-10-369-493-22293 (1-143)

QY 7 TCCGGTGTGCTGTCTGTGATGTGTCATCAAGGTGTTCAACGACATGAAGTGGCTGAAG 66
 |||||
 Db 4 SerGlyValAlaValAlaAspGluSerLeuThrAlaPheAsnAspLeuLys----- 20
 |||||
 QY 67 TCTTCAAGCCAGAGGAGGTGAAGAGCGCAAGAGCGGTGCTCTTCTGCTGAGTGAG 126
 |||||
 Db 21 -----LeuGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 34
 |||||
 QY 127 GACAAGAAGAACATCATCTCGAGAGGCGCAAGAGAGATCCTGTGGGCGATGTGGGCCAG 186
 |||||
 Db 35 AlaLysThrGluIleValValLysGlu-----Thr 44
 |||||
 QY 187 ACTGTGACGATCCCTACGCCACCTTTGTCAAGATGTGCAGATAGAGGATGCGCGTAT 246
 |||||
 Db 45 SerThrAspProSerTyrAspAlaPheLeuGluLysLeuProGluAsnAspCysLeuTyr 64
 |||||
 QY 247 GCCTCTATGATCAACCTATGAGACC-----AAGGAGCAGAGAGGAGGATCTGGTG 300
 |||||
 Db 65 AlaIleTyrAspPheGluTyrGluIleAsnGlyAsnGluGlyLysArgSerLysIleVal 84
 |||||
 QY 301 TTTATCTTCTGGGCCCCGAGTCTGCGCCCTTAAAGAGCAAAATGATTTATGCGAGTCC 360
 |||||
 Db 85 PhePheThrTrpSerProAspThrAlaProValArgSerLysMetValTyrAlaSerSer 104
 |||||
 QY 361 AAGACGCCATCAAGAGAGGCTGACAGGATCAAGCATGAATTCGAAGCAAACTGCTAC 420
 |||||
 Db 105 LysAspAlaLeuArgArgAlaLeuAsnGlyValSerThrAspValGlnGlyThrAspPhe 124

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QY 421 GAGGAGTC 429
Db 125 SerGluVal 127

RESULT 12
US-10-263-255-2
; Sequence 2, Application US/10263255
; Publication NO. US20040191771A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Chua, Penelope
; APPLICANT: Nislow, Corey
; TITLE OF INVENTION: Candida Albicans Cofilin
; FILE REFERENCE: CYTOP072
; CURRENT APPLICATION NUMBER: US/10/263,255
; CURRENT FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Candida Albicans
US-10-263-255-2

Alignment Scores:
Pred. No.: 6,37e-16 Length: 141
Score: 253.50 Matches: 48
Percent Similarity: 60.14% Conservative: 38
Best Local Similarity: 33.57% Mismatches: 36
Query Match: 28.14% Indels: 21
DB: 16 Gaps: 3

US-10-649-952A-2 (1-501) x US-10-263-255-2 (1-141)
QY 7 TCCGGTGTGGCTGCTCTCTGATGTCATCAAGGTGTTCAACGACATGAAGTGCCTAAG 66
Db 4 SerGlyValThrValAlaAspGluSerLeuThrAlaPheAsnAspLeuLys 20
QY 67 TCTTCAACGCCAGAGGAGGTGAAGAAGCGCAAGACGGCGTCTCTTCTGCTGAGTGAG 126
Db 21 -----LeuGlyArgLysTyrLysPheValIlePheThrLeuAsnAsp 34
QY 127 GACAAGAAACATCATCTCGAGGAGGCGCAAGGAGATCCTGTGGCGCATGTGGCCAG 186
Db 35 GluLysThrGlnIleValGluGln-----Thr 44
QY 187 ACTGTGACGATCCCTACGCCACCTTTGTCAAGATGCTCCAGATAAGACTGCCCTAT 246
Db 45 SerThrGluGlnGluTyrAspAlaPheLeuGluLysLeuProGluAsnGluCysArgTyr 64
QY 247 GCCTCTATGATCAACCTATGAGACC-----AAGGAGAGCAAGAGGAGTCTGGTG 300
Db 65 AlaValTyrAspPheGluTyrAspIleGlyGlyGluLysArgSerLysIleVal 84
QY 301 TTTATCTTCTGGCCCCCGAGTCTGCGCCCTTTAAGAGCAAAATGATTTATGCGACTCC 360
Db 85 PhePheThrTrpSerProAspThrAlaProValArgAlaLysMetValTyrAlaSerSer 104
QY 361 AAGGAGCCATCAAGAAGAGTGTGACGGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
Db 105 LysAspSerLeuArgAlaLeuAsnGlyValAlaAspValGlnGlyThrAspPhe 124
QY 421 GAGGAGTC 429
Db 125 SerGluVal 127

RESULT 13
US-10-263-255-4
; Sequence 4, Application US/10263255
; Publication NO. US20040191771A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe

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; APPLICANT: Chua, Penelope
; APPLICANT: Nislow, Corey
; TITLE OF INVENTION: Candida Albicans Cofilin
; FILE REFERENCE: CYTOP072
; CURRENT APPLICATION NUMBER: US/10/263,255
; CURRENT FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-263-255-4

Alignment Scores:
Pred. No.: 3,84e-15 Length: 141
Score: 245.50 Matches: 48
Percent Similarity: 59.44% Conservative: 37
Best Local Similarity: 33.57% Mismatches: 37
Query Match: 27.25% Indels: 21
DB: 16 Gaps: 3

US-10-649-952A-2 (1-501) x US-10-263-255-4 (1-141)
QY 7 TCCGGTGTGGCTGCTCTCTGATGTCATCAAGGTGTTCAACGACATGAAGTGCCTAAG 66
Db 4 SerGlyValThrValAlaAspGluSerLeuThrAlaPheAsnAspLeuLys 20
QY 67 TCTTCAACGCCAGAGGAGGTGAAGAAGCGCAAGACGGCGTCTCTTCTGCTGAGTGAG 126
Db 21 -----LeuGlyArgLysTyrLysPheValIlePheThrLeuAsnAsp 34
QY 127 GACAAGAAACATCATCTCGAGGAGGCGCAAGGAGATCCTGTGGCGCATGTGGCCAG 186
Db 35 GluLysThrGlnIleValGluGln-----Thr 44
QY 187 ACTGTGACGATCCCTACGCCACCTTTGTCAAGATGCTCCAGATAAGACTGCCCTAT 246
Db 45 SerThrGluGlnGluTyrAspAlaPheLeuGluLysLeuProGluAsnGluCysArgTyr 64
QY 247 GCCTCTATGATCAACCTATGAGACC-----AAGGAGAGCAAGAGGAGTCTGGTG 300
Db 65 AlaValTyrAspPheGluTyrAspIleGlyGlyGluLysArgSerLysIleVal 84
QY 301 TTTATCTTCTGGCCCCCGAGTCTGCGCCCTTTAAGAGCAAAATGATTTATGCGACTCC 360
Db 85 PhePheThrTrpSerProAspThrAlaProValArgAlaLysMetValTyrAlaSerSer 104
QY 361 AAGGAGCCATCAAGAAGAGTGTGACGGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
Db 105 LysAspSerLeuArgAlaLeuAsnGlyValAlaAspValGlnGlyThrAspPhe 124
QY 421 GAGGAGTC 429
Db 125 PheGluVal 127

RESULT 14
US-10-424-599-186070
; Sequence 186070, Application US/10424599
; Publication NO. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 186070
; LENGTH: 139

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US-10-0229-386-30107

Alignment Scores:
Pred. No.:      1,02e-13      Length:      60
Score:          230.00        Matches:     43
Percent Similarity: 89.66%    Conservative: 9
Best Local Similarity: 74.14% Mismatches:   6
Query Match:      25.53%     Indels:      0
DB:               14         Gaps:        0

US-10-649-952A-2 (1-501) x US-10-029-386-30107 (1-60)

Qy      130  AGAAGAATCATCTCTGAGAGGGCAAGGAGATCTCTGGTGGCCGATGGGCCACGACT 189
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1   LysLysCysIleIleValGluGluGlyLysGluIleLeuValGlyAspValGlyValThr 20

Qy      190  GTCCAGCATCCCTACGCCACCTTTGTCAGATGCTGCCAGATAAGCACTGCCGCTATGCC 249
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      21  IleThrAspProPheLysHisPheValGlyMetLeuProGluLysAspCysArgTyrAla 40

Qy      250  CTTCTATGATGCCAACCTPATGAGACCAAGGAGAGCAAGAAGGAGGATCTCGTGTGTTT 303
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      41  LeuTyrAspAlaSerPheGluThrLysGluSerArgLysGluGluLeuMetPhe 58

Search completed: May 13, 2005, 10:05:21
Job time : 108.5 secs

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